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GenCore version 4.5
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nucleic search, using sw model owner of the second

Run on:

August R. 2001, 19-26-67 program time per 64 Seconds (Without alignments) 3752.043 Million cell apdates/see

US 99 475 794 4 1509 Title: Perfect score:

. godgev elettgagekagtaa 1509 l afgggggggggggggggggggg IDENTITY_NUC Sapop 10.0 , Sapext 1.0 Scoring table; Sequence:

lotal number of hits satisfying chosen parameters:

740101 seqs, 413550809 residues

Sear ched:

Minimum DB seq length: 0 Maximum DB seq length: 269099990

Listing first 45 summaries Maximum Match 190% Post-processing: Minimum Match 0%

batabase :

N. dencorq_0691:•
- /cqn1_g/oroqtana/qencorq/qencorqp/NN1940_1ATC•
- /cqn1_g/oroqtana/qencorqp/pencorqp/NN1941_1ATC•
- /cqn1_g/orqdata/qeneseq/qencorqp/NN1962_DATC•

/cqn1_9/qcqdata/geneseq/qeneseqn/NA1996.DAT:*

/eqn1_9/gegdata/geneseq/qeneseen/NA1997_DAT.* /eqn1_9/qeqdata/qeneseq/qeneseqn/NA1998_DAT.* /eqn1_9/te-qdata/peneseq/qeneseqn/NA1999_DAT.* /eqnl_9/qeqdata/qeneseq/qeneseqn/NA2001.DAT:* Zagnij jezh gdatazapenesegzpenssegnyNA2600 144T 🖈

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Score	Match	Ouery e Match Length DB ID	E H	115	Description
ı	6051	1509 100.0	1509	21	AAA51610	HIV synthetic Gag
-	489.8	9.B. 7		3	AAA51626	HIV codon optimize
T	8.912	₹ 1276.8 84.6		2.1	AAA51609	HIV synthetic Gag
	8.03	84.6		ā	AAA51625	HIV coden-optimize
	1071			[]	AAA70412	Synthetic HIV Gag
	1201			៊	AAA70472	HIV bicistronic co
	1201			-,	AAA 2 0 4 7 3	HIV bicistronic co
	1201			2.1	AAA70471	HIV bicistronic co
	1.701			2.1	AAA70470	HIV bicistronic co
	1199	79.5	2031	ći	AAA79415	Synthetic HIV Caq/
-	117.8	74.1		ā	AAA70414	HIV Gag-brotease e

HIV Gag-protease e	HIV Gag-profease e	HIV Gaq-polymerase	Codon optimised Bu	Packaging construc	HIV Gag common reg	Humanised HIV-1 da	Synthetic HIV dag	HIV qaqpol SYNqp C	Human immunodelici	Nacleatide sequenc	HIV partial leader	HIV partial leader	HIV complete leade	Humanised HIV-1 qa	HIV-1 non-subtype	HIV-1 non-subtype	HIV-1 non-subtype	RIV 1 non-subtype	Complete sequence	HIV-1 non-subtype	HIV-1-JC infection	HIV-1 dag protein	Wild type Human im	HDPACK1. Human im	HDPACKI DNA constr	BIV-l proviral elo	HIV-1 NL4-3 genomi	Nucleic acid seque		MIV-1 viral protei	ARV 1 NEZHIB FOC	Vector pHP-1 compr	Flasmid pNLmSG11 e
AAA70475	AAA70476	AAA70414	AA252051	AA252055	AAA70417	AAF31284	AAV45174	AAZ08740	AAA94972	AACB6876	AAA9 1984	AAA93983	AAA9 8982	AAI' 41286	AAP57927	AAF57929	AAF57926	AAF57922	AA006635	AAF57919	AAX0 3986	AAV35386	AA252050	AAQ33479	AAVOR704	AAQ22488	AAQ96140	AAVH1H71	AAA97926	AAA4 11298	AA481	AAVB 1206	AAV14355
៊	2.1	7.1	2	21	21	22	13	0.7	53	C1 C1	ឧ	៊	<u>-</u>	검	54	23	 	ā	11	គ	20	5	51	-	2.0	23	16	2.0	53	5	:;	្ន	18
1865	1865	4319	1503	8368	1268	1532	1630	4307	4 ±07	4 3 0 7	4 +27	4353	46.12	1482	8972	0968	6006	2668	9143	8368	9193	1503	1503	7399	7 499	6026	6076	4709	6076	5025	6.57	12494	15581
74.1	74.1	74.1	71.4	71.4	69.5	64.4	64.3	61.6	61.6	9:19	61.4	61.3	61.3	60.7	48.7	47.0	47.0	44.0	43.3	다. 전	42.8	42.6	1 2.6	42.6	42.6	9 . E	42.6	42.6	42.6	42 E	-:-	42.6	42.6
1117.8	1117.8	1117.8	1077.4	1077.4	1049-2	971.4	9.696	930.2	930.2	930.2	925.4	925.4	#1000 0000	916.6	734.2	709.6	709.6	9.8.99	654	651.8	646	642.2	040.0	642.2	642.2	642.2	642.2	642.2	642.2	642.2	5.12.2	542.2	542.2
15	1.3	14	15	16	17	3.6	ž	0.7	ē.	04 04	ã	\$3	un Ca	9.7	27	58	53	3.0	31	.: 1	3.3	34	67	36	3.7	38	39	40	41	ं च	÷	***	.i)

ALIGNMENTS

AAA51610 standard: DNA: 1509 BP. AAA51610 RESULT

AAA51610;

31 -47:2000 (first entry)

HIV synthetic Gag polynucleotide.

Cas, expression exserts, attidents, type C, HIV, Enc, synthetics PNA immenication, packaging cell line, antique presentation; ss.

Human immunodeficiency virus type C strain AF110967. Synthetic.

W0200039304-A2.

06-JUL-2000.

99WO-US31273. 80-DEC-1999; 11-DEC-1998;

98US-0114495. 99US-0152195. 01-SEP-1999;

(CHIR) CHIRON CORP.

Barnett S, Zur Megede J;

MP1: 2000-452401/39.

Polynucleotide encoding antiqenic type C HIV Gag polypeptide or a HIV Enr polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV

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                                                                                                                                                                                                                                                                                                                                           production of Gag- and/or Env-containing proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of cytotoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iif-assemble into non-infectious virus-like particles which are used as matrix for the proper presentation of an antigen entrapped or
                                                                                                                                                            Expression cassettes comprising a polynuclectide encoding antigenic type C human immunodeficiency virus (HIV) Gag or Env polypeptides are useful in DNA immunization, generation of packaging cell lines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 geogacagocaaagttgagecagaactaceccatcgtgcagaacetgcagggccagatggtg 420
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                                                        Claim 2; Page 93; 113pp; English.
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Expression cassettes comprising a polynucleotide encoding antigenic type c human immunodeficiency vicus (HTV) Gag or Env polypeptides are useful in DNA immunisation, generation of packaging cell lines and production of Gag- and/or Env-containing proteins. Synthetic Env and Cag expression cassettes exhibit increased potency for induction of cytoxoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-assemble into non-infectious vilus-like patiticles which are used as a matrix for the proper presentation of an antigen entrapped or associated to the immune system of the host.
                                                                                                                                                                                                Codon usage pattern was modified and inhibitory elements (INS) and RRE sites were inactivated resulting in improved expression"
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                             Gag; expression cassette, antiqenic, type C, HIV, Env; synthetic; DNA immunization; packaging cell line; antigen presentation; ss
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                                                                                 Human immunodeficiency virus type C strain AF110965.
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HIV synthetic Gag polynucleotide
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Similarity 92.5%;
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production of Gaq and/or Env-containing proteins. Synthetic Env and Gag expression easestrus exhibit increased potency for induction of expression cassetty exployer (CTL) responses by INA immunization, Gag of HIV-1 self-assemble into one infortions virus like particles which are used as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expression cassettes comprising a polynucleotide encoding antiqueic
                                                              Gag: expression cassette; antiqenic; type C; BIV; Env; synthetic;
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                                                                                                                                                                                                                                                                                                                                                 HIV codon-optimized synthetic Gag polynucleotide.
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87; Indels

Pred. No. 3.3e~149; 0; Mismatches 87;

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Matches 1389; Conservative

Best Local Similarity

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Sequence 1515 BP; 329 A; 547 C; 480 G; 159 T; 0 other;

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1198 aactgccqcgcccccqcaagaaggctgctggaagtgcgggaaggaggccaccagatg 1257
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                                                                                                                                                                                                                                    1420 g-----accgcgagaccctgaccagcctgaagagcctgttcggcaacgaccc 1467
1138 aagggeeeecycegeategtgaagtgetteaactgegeaaggaagggeeeategeeege 1197
                                             1198 aactgeeyeyseesessaayaayyyetyyaaytyeyysaayyyayyyyeeseyatta 1257
                                                                     1258 aaggactgcaccgagcgccaggccaacttcctgggcaagatctggcccagccacaagggc 1317
                                                                                           1258 aayyantynannyaynynnagginnäänttinntyggnäägatiitygsninagneanaagger 1317
                                                                                                                  1318 egeceeggeaactteetgeagaacegeagegegeegeegeegeegeegegtgeeeagtgeeeaegt
                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic HIV Gag expression cassette coding sequence Gag.ModSF2
                                                                                 Srivastava I, Lian Y, Hartog K,
                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV-1; AIDS, Gay, vaccine, expression cassette, ss.
                                                                                                                                                                             Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                            1498 ctqaqccaqtaa 1509
                                                                                                                                                                                                                                                                                  1468 ctgagccagtaa 1479
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The present sequence is the coding sequence of a HTV Gag expression cassette, Gag.McdSF2. The Gag prittin of HTV is cashed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HTV life cycle, including assembly, virion maturation after particle release and early post entry stages in viral replication. The expression cassette may be used for the recombinant expression of HTV Gag-polypeptides which may then be used to vaccinate against HTV

infection and acquired immunodeliciency syndiome (Albs).

Expression cassettes encoding the human immunodeficiency virus (HIV)

Gaq-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -

Claim 3; Fig 7; 391pp; English.

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646 caggeoggeocogtggeocoggeoagatgegegaceecogyggaagegaatgegggg 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 caggqccagatq4tgcaccaggccatcagccccgcacctgaargrrtgggtgaaqatg 465
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dby M, Walker C;
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                                                                                                    The present invention relates to synthetic HIV Gap and Env expression vassettes. The Gap protein of HIV is needed for the assembly of virus-like particles. In addition, the Gap protein is involved in many stages of the HIV like eyele, including assembly, virion maturation after particle release and early post entry steps in viral replication. The expression easeltes may be used to the tereshelmed expression of HIV intestion and Env-polypeptides which may then be used to varctimate against HIV intestion and addited inmanodeticiency syndrome (ALDS). The present sequence is a synthetic construct constructed in the generation of the expression cassettes of the present invention. This construct is bicistronic in that the coding sequences for Env and Gap are under the control of a single CMV promoter and between the two coding sequences an
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                                                                              3959 eccycygecaenriggaggaggaggatgatgaecycetyceaqqqeatqaqquaececqqeeae 4018
                                                                                                                                                                                                                                                                          1066 aaggeeegegtgetggeegaggegatgatgageer esaacagegtgaacateatgatg 1122
                                                                                                                                                                                                                                                                                                   4019 aaggeeegeytgetggeegaggegatgageeaggtgaegaaeeeggegaeeateatgatg 4078
946 gagaccetgetggtgcagaacgccaaccccgactgcaagaccatectgcgcgctctcggc 1005
                                                                                                                                                                                                                             1006 ringgrandargaaggagataataacaccaccagagaaqaqacacagccac 1065
                                                                                                                              886 egettetteaagacettgegegeegaagacaceaagacatgaagaactgaatgace 945
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                                    766 ggegaeatelaeaageggtgateāteetgggeetgaacaagategtgeggatgtacage 825
                                                                                                                                                                                                                                           HIV bicistronic construct gp160.modSF162.dr1V2.Gag.modSF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV-1; AIDS; Gag; vaccine; expression cassette; Env;
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The present invention relates to synthetic HIV Gag and Env expression cassettes. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post entry Steps in viral replication. The expression cassettes may be used for the recombinant expression of HIV gag- and Env-polypeptides which may then be used to vaccinate adminst HIV infection and acquired immunodeficiency syndrome (AIDS). The present sequence is a synthetic construct constructed in the generation of the variesisten cassettes of the present invention. This construct is bisistronic in that the coding sequences for Env and Gag are under the control of a single CMV promoter and between the two coding sequences an Internal Ribosome Entry Site (IRES) is present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1255 etgggccagetgcageccagectgcagaccggcagaggaggaggetgcgcagcctgtacaac 3314
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                                                                                                                                                                                                                                                             Expression cassettes encoding the human immunodeticiency virus (HIV) Gaq-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
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                                                                                                                                                          Sur Megede J, Srivastava I, Lian Y, Hartog K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4608 BF, 1001 A; 15MP P; 1382 G; 645 T; 0 other;
                                                                                                                                                                                                                                                                                                                                               Claim 19; Fig 64; 391pp; English.
                                                                                                                                                                                        Greer C, Selby M, Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ijarity 88.5%;
Popsorvative
                                                                       98US-0114495
                                                                                           440S-0168471.
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Matches 1951, Posserva
                                                                                                                                 (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                               WPI; ZUUU-4524UU/39.
                                      30-DEC-1999;
06-JUL-2000
                                                                                                                                                                          Bainett S,
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5 3	1124	cadaatan anctikodagddoc ocqqoordaagdd raagtgothodactgogqodaagdd H	1182 4274
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The present invention relates to synthetic HIV Gaq and Env expression cassettes. The Gaq protein of HIV is needed for the assembly of virus-like particles. In addition, the Gaq protein is involved in many stages of the HIV life eyele, including assembly, virice maturation after particle release and early post entry steps in viral replication. The expression cassettes may be used for the recombinate expression of HIV caq- and Env-polypeptides which may then be used to vaceinate against HIV intertion and acquired immunodeliciency syndrome (ALDS). The present sequence is a synthetic construct constructed in the generation of the expression cassettes of the present invention. This construct is bicistronic in the coding sequences for Env and Gaq are under the reality side expressed or a single ENV promoter and between the two coding sequences an internal Ribosome Entry Site (IRES) is present.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression cassettes encoding the human immunodeficiency virus (HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.6%; Score 1201; DB 21; Length 4689;
88.5%; Pred. No. 6.9e 142;
live 0; Mismatches 140; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dag-containing polypeptide useful for vaccinating against HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4689 BP; 1029 A; 1606 C; 1397 G; 657 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infections and acquired immunodeficiency syndrome (AIDS)
                                                                                                                                                                                                     HIV-1; AIDS; Gaq; vaccine; expression cassette; Env; ss
                                                                                                                                                             HIV bicistronic construct qp160.modUSF162.Gag.modSF2.
                                                                                                                                                                                                                                            Chimeric - Cytomedalovirus.
Chimeric - Human immunodoticiency virus type 1.
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                                        AAA76471 standard; DNA; 4689 BP.
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                                                                                                                         (first entry)
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Best Local Similarity 88.5%
Matches 1351, Conservative
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                                                                                                                     28-NOV-2000
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Greer C, S
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                     AAA70471
RESULT
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3336-ctqqqqccagctycaqrccagcrtqraqaccyqyraycqayqaqctqvqcaqcctqtacaac-3395

QY	acctggccaccctgtactgcgtgcacgccggcatcqaggtccgcgacaccaaqgaggcc 300
pp	96 accytyyecaectytactgcgtgcaccagcgcatcgacgtcaaggacaccaaggaggrr 44
Qy	01 ctggacaagatcgaggaggagcagaacaagtcccagcagaagacccagcaggccaa
q	56 otyyvaydagateyayyaygayeugaacaagteeaaqaagaagaagaegeeagaggeenagaaggeeseagaaggeeseagaaggeesea
oy 4	361 geogaeggear
g G	Ib geogeogggeacoggeageageageageageegeegeegeegeegeegeegee
oy de	
2 0	466 atcaagaaagacetteageeeegagqtgateeecatgtteaeegeeetgagrgagge 525
, a	6 gtggaggagaagccttcagccccgaggtgatccccatgttcagcgccctgagcgagggc 3
çy	526 georgeocoaggacotgaacacgatgttgaacacogtgggcogcoacaggcogcoatg 58
qq	
δy	86 cagatgctgaaggacaccatcaacgaggaggccgccgagtgggaccgcctgcaccccqtg 645
qq	6 cagatgotgaaggagaccatcaacgaggaggccgccgagtgggaccgcgtg
Ωy	6 caggeoggeoggiggoconogocagatgogogacocoqoqqoqqoqqoqqtogooggo 705
qq	ngccccggccagatgcgcgagcccqcqqqcagcgacatcgccggc
ς	e gecaceagearritgiaggagragategortggatgaecaaceacececettgeegtg 765
qq	6 accaccagcarritgraggagcagatrggniggitgatgaccaacaacacccccatcccqtq
ΟŊ	s ggcgacatctacaagcgglggalcalcclgggcclgaucaagalcgtgcggalgtacagc 825
qu	36 ggcgagatctacaagcggtggatcatcctgggcctgaacaagatcgtgcggatgtacagc
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Qy	1303 occaqueacaayyqcegeceggeaacttectgeagaacogeayeqayeegeegeece
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Qy Db	1423 aagcaggageeennygnnogegageeetadeggageeeetgaeeggeetgognagnotg 1482 111 11 11 11 11 11 11
Qy Db	1483 tteggeagegereretgagecaqtaa 1509
RESULT AAA7047 ID AA	11.T 9 10470 AAA70470 standard; DNA: 4766 BP.
X X	AAA70470;
X L	28-NOV-2000 (first entry)
DE X	HIV bicistronic construct gp160.modUS4.Gag.modSF2.
X X	HIV-1; AIDS; Gag; vaccine; expression cassette; Env; ss.
s os	Chimeric - Cytomegalovirus. Chimeric - Human immunodeficiency virus type 1.
X A	W0200039302-A2.
ΧΞ	ψε-40L-2000.
XX PF	30-DEC-1999; 99WO US31245.
XXXX	31-DEC-1998; 98US-0114495. 01-DEC-1999; 99US-0168471.
X ~	(CHIR.) CHIPON CORP.
X d d	Barnett S, Zur Megede J, Srivastava I, Lian Y, Hartog K, Liu H; Greer C, Selby M, Walker C;
ΧΫ́	WPI; 2000-452400/39.
Z Z Z Z	Expression cassettes encoding the human immunodeficiency virus (HIV) Gaq-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndiome (AIDS) -
× S	Claim 27; Fig 61; 391pp; English.
X C C	The present invention relates to synthetic HIV Gay and Env expression cascattes. The Gay protein of HIV is needed for the assembly of
36	virus-like particles. In addition, the Gay protein is involved in mary stages of the HIV life cycle, including assembly, virion maturation after
38	particle release and carly post Ontry Steps II Vital reprisersion expression cassettes may be used for the recombinant expression of HIV
35	Gag- and Env-polypeptides which may then be used to vaccinate resemble infection and acquired immunodeficiency syndrome (AIDS). The present
888	sequence is a synthetic construct constructed in the generation of the expression cassettes of the present invention. This construct is expression cassettes of the present invention.
3 E E	Dicistronic in that the couling sequences to the two coding sequences an control of a single CMV promoter and between the two coding sequences an internal Ribosome EnLFV Site (IRES) is present.
XX XX	Sequence 4766 BP; 1051 A; 1038 C; 1409 G; böß 1; 0 other,

Query Match 79.6%; Score 1201; DB 21; Length 4766; Best Local Similarity 88.5%; Pred. No. 6.9e-142;

ž	Matches 1351; Conservative 0	0; Mismatches 140; Indels 36; Ga	Gaps 3;		
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present sequence was cloned and used to generate the expression cassettes of the present invention. The expression cassettes may be used for the recombinant expression of HIV Gaq-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome
                                                            stages of the HIV life cycle, including assembly, virion maturation after particle release and early post entry steps in viral replication. The present invention relates to synthetic HIV Gag expression cassettes. The
virus-like particles. In addition, the Gag protein is involved in Many
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Best Local Similarity
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                 HIV-1; AIDS; Gag-protease; vaccine; expression cassette; ss
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· · The present sequence is the coding sequence of a HIV Gag-protoase expression cassette, GagProt ModS. The Gag protein of HIV is næded for the assembly of virus-like particles. In addition, the Gag protein is invested is many states of the HIV like eyele, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag polypeptides which may then be used to vacchiate against HIV intection and acquired lammandeliciency syndrome (ALES). 61 ofgegerenggegaagaagaan arafgetgaagaaretgaagaaretgg. 67 intigegeonegginggesagaagaagtacaagnigaageanatingtigtgggeeageegegag 126 12) etggaggettegeeetgaaceeeggeetgetggagaeegeegagggetgeaageagate 180 187 etaggecageturayeetgeetgeetgeagaeeggeageggagetgegeageetgtacaae 245 401 et aquecaaqui equaquaquageaqaaetaqi ecceaqeaqaaqeaqqaqqaq 360 - ELLE ELLE 367- grogorga assign-ansagsags agattgags bagaastarcrategtgeagaaceta 426 427 ragggecagatugtgeaceaggeeateageeegeaeeetgaaeegeetgggtgaaggtg 486 geranceri vayyaretygaeacaeyatyttyaanacegtyyyrygecaecaggeogecatg 606 586 - caqatigotidaaggaraccatoaacgaggaggacgecgagtyggaccgectgeacegty - 645 Expression cassottes enoughry the human immunodeficiency virus (HIV) 247. annytyyyniannetytantynytysannaynyvatryanythiaayyadaccaaggaggod 127 et ggagegettegeegtgaaneengeetgetgagaaeagggggetgeeggeegate 18] at qaagcaqet geageeegeeetgeaqaeeggeaeegaqqaqetgegeageetgtacaae accepted accepted the transfer of the accepted and the control of 307 intiggagadatingaggaggaggagagagtonaagaagagguoggoogoogoo 461 geogacogress some additional according to a grant and a grant and a grant and a grant a gr 487 intiquaggadaaggeent teageneegaggigateeecalgiiteagegeetgagegagge geracemenagaint gaarapgat qt tigaacaecqtyqqqqqqciain aggecyneitig Ouery Match 74.1%; Score 1187.8; DB 21; Length 1853; Hest Local Similarity 85.1%; Pred. No. 1.7e-141; day containing polypeptide useful for vaceinating against HIV intections and acquired immonodeticiency syndrome (AIDS) -Srivastava I, Lian Y, Hartog K, 0; Mismatches 192; Indels Sequence 1853 BP; 421 A; 624 C; 580 G; 228 T; 0 offser; Claim 5; Fig 7; 391pp; English. Greer C, Selby M, Walker C, Zur Megede 17 Conservative (CHIR.) CHIRON CORP. WPI: 2000-452400/39. Matches 1299; Barnett S, ÷ 3 â 5 å ें 3 3 Ξ 3 3 5 3 S £ Š 4 5 3

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HIV Gaq-protease expression cassette coding sequence GagProtMod.SF2(GP1).
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The present sequence is the coding sequence of a HIV Gag protease expression cassetto, GagProtMod.SF2 (GPI). The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome
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Pred, No. 1.7e 131;
0; Mismatches 192: Indels
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Human immunodeficiency virus type 1.
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Similarity 85.18;
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466 alogagagagagtotosporovaggiqaloocoatgifosovapootgagogaggac
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HIV Gay professe expression cassette coding sequence GagProfMod.SF2(GP2).
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vaccinate against HEV infection and acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the coding sequence of a HIV Gay protease expression cassette, GagFrotMod.SP2(GP2). The Gag protein of HIV is needed for the assembly of virus like particles, in addition, the Gay protein is involved in many stages of the HIV lite eyele, including assembly, virion maturation after particle release and carry post votry steps in viral replication. The expression cassette may be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Zur Megede J. Srivastava I, Lian Y. Hartog K, Liu H;
Selby M. Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression cassettes encoding the human immunodeficiency virus (BLV) day containing polypeptide useful for vaccinating against HLV infections and acquired immunodeficiency syndrome (AIDS)
                                                                                                                                                                        BIV 1: ALDS; Gag-proteuse; Vaccine; expression cassette; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1865 RP; 460 A; 583 C; 569 G; 253 T; 0 other;
                                                                                                                                                                                                               Human immunodeticiendy virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Fig 70; 441pp; English.
                  AAA70476 standard; DNA; 1865 BP
                                                                                                                                                                                                                                                                                                                                                   99WO-11S31245
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                                                                                             28-NoV-2000 (first entry)
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                                                                                                                                                                                                                                   Syntheric.
                                                        AAA70476;
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AAA70476
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121 ottagaaqqettoqeetqaaceeqqeetqetqaaceeqeeqaaqqetqeaaqeagate 180 181 af qaaqraqet qeaqeeegeeet qeaqaeeqqqeaeeqaqqaqet qeqeaqeet qtaeaaae 240 24] accytygerarentyfantgegtgeacyccygnategagyteegacaceaaggagge 300 61 in the group appropriate and a start grant of the appropriate of the start of the appropriate of the start of the appropriate of the appropriat 73 ct.gegeeerggeggaagaagtacaagaagtacaagcacategtgtggggeeageegag 132 133 ortugagogoticgcogidaacconggootgeigaagaacaagaagagotgoogooagate 192 1931 of gggm age the agestrates by agading agading agaging agglaguaged by tadaal. 252 13 attagegerengegerengentgetgageggegggeriggaeaagtgggagaagateege 72 36; Gaps Ouery Match 74.1%; Score 1117.8; DB 21; Length 1865; Best Local Similarity H5.1%; Pred No. 1.7e-131; 0; Mismatches 192; Indels Matches 1299; Conservative

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oy Dp	1123	cagaagaycaactt caagaaccccqyracaacgi caastyett caact acggcaaqaa 	1182
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5 6	1333	cettectacaaqqqaaqqecaqqqaattttettaqaqqqa	1.374

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The present sequence is the coding sequence of a HIV Gaq-polymerasc expression cassette, GaqPol.ModSF. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle repleated may be used for the recombinant expression cassette may be used for the recombinant expression of HIV dag pulypeptides which may then be used to varining against HIV infection and acquired immunodeficiency syndrome (AIDS).
                                                             1423 aagraggagnecaaaggacogngageectacegergageneertganngenntdegeacetg 1482
                   1363 accytycecaccycececeyecyayayatt.ccycttcgaggagaccaccccgcccc 1422
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sıby M, Walker C;
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                                                                                                                                                                                                                                                                                                                                                HIV Gag-polymerase expression cassette coding sequence GagPol.ModSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
                                                                                                                                                                                                                                                                                                                                                                                   HIV-1; AIDS; Gag-polymerase; vaccine, expression cassette, ss.
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                                                                                  1483 ttcggcagcggcccctgagccagtaa 1509
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                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
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99US-0168471.
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01-DEC-1999;
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36: Gaps

192; Indels

Mismatches

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Conservative

Best Local Similarity Matches 1299; Conserv

Query Match

74.1%; Score 1117.8; DB 21; Length 4319; 85.1%; Pred: No. 1.5e-131;

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1087 aaggeeegegtgetggeegaggegatgageeaggtgaegaaeeeggegaeeateatgatg 1146
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67 etgegececggegaagaagaagtacaagetgaageacategtgtgggeeageegegag 126
                                      127 ctggagegettegeegtgaaeeeeggeetgetggagaeeagegagggetgeegeeagate 186
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The patent discloses new packaging cell line for producing a viral accessory protein independent lentivirus, preferably human immunodeticiency virus (HIV), derived retroviral vector particles.
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                                                                                                                                                                                                                                                              1423 liadacia-ppagnin aaqqaningegaginistar eginyaqeeletyaeeqwinitgegeageetig. 1482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qene therapy; gene replacement; vaccine; biochemical reagent;
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12 SEP - 1998;
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The present sequence is a gas coding region of codon optimised HIV adapped sequence. This sequence is used in the packaging sequence is each line. Codon optimisation results in improved expression of the gagpol projet in and reduces the risk of recombination between the transfer
The packaging cell line comprises a mammalian cell, a retroviral DNA comprising a coding sequence for a refliction, preterably HIV, gaspol, where the coding sequence has been mutagenised to improve expression of the viral gaspoi proteins, a second retroviral mucleotide sequence comprising the coding sequence for a heterologous envelope protein and a
                                                                                                                                                                                                                                                                                                                                                                                     They can also be used
                                                                                                                                                                                                                                                                                                                                        The packaging cell lines and viral particles can be used for gene therapy of gene replacement with improved safety. They can also be used in the development and production of varcines and biochemical reagents.
                                                                                                                                                                                                            third retrovital moefectide sequence comprising a DNA sequence of
interest and lentivitus, preterably HIV, cis acting sequences required
for packaging, reverse transcription and integration.
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84.5%; Pred. No. 1.9e
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Matches 1270; Conservative
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Search completed: August 8, 2001, 18:26:48 Job time: 12712 sec

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Perfect Score: Sections

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Scoring table:

730101 seqs, 313950809 residues Gapop 10.0 , Gapext 1.0 Sear ched:

Fotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000600000

Listing first 45 summaries Maximum Match 100% Post processing: Minimum Match 0%

Latabase :

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result being printed, Prod. No. is the number of results predicted by chance to have a and is derived by analysis of the total score distribution. score greater than or equal to the score of the

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SUMMARIES

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Result	Score		Goorty Match Length DB - ID	EDB	11	bescription
_	113		900	2.1	AAA51607	HIV Gaq major homo
7	6.0	100.0	1479	21	AAA51609	HIV synthetic Gag
~	09	100.0	1479	7	AAA51625	HIV codon-optimize
4	2,27		09	[2	AAA51608	HIV Gag major homo
C.	55.2	92.0	1509	2	AAA51610	HIV synthetic Gag
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AAA51607 standard; DNA; 60 BP. 31-OCT-2000 (first entry) AAA51607; AAA51607 PUSULT $\begin{array}{c} \mathbf{x} \oplus \mathbf{$

HIV Gag major homology region nucleotides 844-903.

day, expression cassette, antiquie; type C; HIV; Env; synthetic; EAA observators to, pertuang cell time, antique presentation, 88.

Human immunodeficiency virus.

WO200039304 - AZ.

06-JUL-2000.

99WO-US31273. 40-DEC-1999;

9908-0152195. 980S-0114495. 41-DEC-1998; 01-SEP-1999;

(CHIR) CHIRON CORP.

Barnett S, Zur Megede J;

WPI; 2000 452401/39.

Polynucleotide encoding antiquate type C HIV dag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV

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Gaps

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Expression cassettes comprising a polynucleotide encoding antigenic type c human immunodeficiency virus (HIV) Gag or Env polypeptides are useful in DNA immunization, generation of packaging cell lines and production of Gag- and/or Env-containing proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of cytotoxic I-lymphocyte (CTL) responses by DNA immunization. Gag of HIV 1 self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antigen entrapped or associated to the immune system of the host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a /*tag= a /product= Synthetic_Gag /product= Codon usage pattern was modified and inhibitory /note= "Codon usage pattern was modified and inhibitory recedence (INS) and RRE sites were inactivated resulting in improved expression"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expression cassettes comprising a polynuclectide encoding intigenic type C human immunodeficiency virus (HIV) Gag or Env polypeptides are useful in DNA immunization, generation of packaging cell lines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide encoding antiqenic type C HIV Gag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV
                                                                                                                                                                                                                                                                                                                       Gag; expression cassette; antiyenic; type C, HIV, Env; synthetic; DNA immunization; packaging cell line; antigen presentation; Ss.
                                                                                                                                                                                                                                                      100.0%; Score 60; DB 21; Length 60; 100.0%; Pred. No. 1.5e-10; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                      Sequence 60 BP; 14 A; 22 C; 15 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                          0; Mismatches
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Claim 1; Paye 92; 113pp; Euglish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV synthetic Gag polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA51609 standard; DNA; 1479 BP
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                                                                                                                                                                                                                                                                                          60; Conservative
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                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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production of Gag- and/or Env-containing proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of explosive T-lymphoxyPe (CTL) responses by DNA immunization. Gag of HIV-1 self-assemble into morn infectious virus-like particles which are used as a matrix for the proper presentation of an antigen entrapped or
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DNA immunization; packaging cell line; antigen presentation, ss.
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                                                                                                                                                                                     Length 1479;
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                                                                                                                                 Stappenson 1479 BP, 325 A, 529 C, 463 G, 162 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type C strain AF110965
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                                                                                                                                                                                     100.0%, Score 60, DB 21, 100.0%, Pred. No. 2.1e-10; tive 0, Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                        AAA51625 standard; DNA; 1479 BP.
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                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 60; Conservative
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Expression casseties comprising a polynucleotide encoding antigenic type C human immunodeliciency withs (HV) Cag or Enr polypeptides are useful in DNA immunization, generation of packaging cell lines and production of Gag- and/Arr Piv containing proteins. Synthetic Env and expression casseties exhibit increased potency for induction of evicotoxic T lymphocyte (CTL) responses by DNA immunization. Gag of HIV-3 self-assemble into non-infections virus-like particles which are used as a matrix for the proper presentation of an antique entrapped or
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0; Gaps
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Matches 57; Conservative
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Expression cassettes comprising a polynucleotide encoding antiquency type C human immunodeficiency virus (HVV) Gag or Env polypeptides are useful in DNA immunization, generation of packating cell lines and production of Gag and/or Env-containing proteins. Syntheric Env and Gag expression cassettes exhibit increased potency for induction of expression cassettes exhibit increased potency for induction of expression cassemble into non-interficus virus like particles which are used as a matrix for the proper presentation of an antiquen entrapped or
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expression cassette, autiquaic, type C, HiV; Env; synthetic;
                                   DNA immunization; packaging cell line; antigen presentation; ss.
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                                                                                               Human immunodeficiency virus type C strain AFI10967
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Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barnett S. Zur Megede J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR ) CHIRON CORP.
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                                                                                                                                      Synthetic.
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                                                                                                                                                                       type c human immunodefichency virus (HIV) day or Env polypeptides are useful in DNA immunotation, generation to packaging cell lines and production of Gay—and/or Env-containing proteins. Synthetic Env and Gay expression cassettes exhibit increased potency for induction of cytocoxic T-lymphocyte (CTL) responses by DNA immunization of self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antigen entrapped or
                                                                                                                                                                                                                                                                                                                                                                                   /product= "HIV p55 Gag Major Homology Region protein"
/note= "No stop codon given"
                                                                                       Polynucleotide encoding antigenic type C HIV Gag polypeptide of a HIV
                                                                                                                                                                                                                                                                                                                                                  0; Caps
                                                                                                                                                                                                                                                                                                                                                                          1 qacatcaagcagggccccaaggaqcccttccgcgactacgtggaccgcttcttcaagacc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Zur Megede J, Srivastava I, Lian Y, Hartog K, Liu H;
Selby M, Walker C;
                                                                                                                                                                Expression cassettes comprising a polynucleotide encoding antigenic
                                                                                                 Env polypeptide and the polypoptide useful for immunizing a mammal especially human against HIV
                                                                                                                                                                                                                                                                                                                      92.0%; score 55.2; UB 21; Length 1509;
95.0%; Fred. No. 6.9e-09;
Live 0, Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                    Sequence 1509 BP; 321 A; 559 C; 471 G; 158 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV-1; AIDS; Gag; vaccine; expression cassette; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV p55 Gag Major Homology Region coding sequence.
                                                                                                                                                                                                                                                              associated to the immune system of the host.
                                                                                                                                        Disclosure: Page 104; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA70426 standard; DNA; 60 BP
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Matches 57; Conservative
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                                         Barnett S, Zur Megede
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               (CHIR ) CHIRON CORP
                                                                WPI; 2000-452401/39
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The gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle classette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                               The present invention relates to synthetic HIV Gay expression cassettes. The Gay protein of HIV is needed for the assembly of virus-like particles. In addition, the Gay protein is involved in many stages of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to synthetic HIV Gaq expression cassettes.
                                                                                                                                                                                              HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV (Gaq-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS). The present sequence is the coding sequence of HIV p55 Gag Major Homology Region. This sequence is located within the p24 CA sequence of Cag. Mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
Expression cassettes encoding the human immunodeficiency virus (HIV) Gaq-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
Local Similarity 93.3%; Score 53.6; DB 21; Length 60;
Local Similarity 93.3%; Pred. No. 1.6e-08;
les 56; Conservative 0; Mismatches 4: Indels (
                                                                                                                                                                                                                                                                                                                                                      this region can severely impair particle production.
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 60 BP; 13 A; 24 C; 15 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV Gag common region coding sequence.
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                                                                                             Claim 1; Page 345; 391pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA70417 standard, DNA; 1268 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0114495.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200039302-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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human immunodeticiency viras (HIV), derived retroviral vector particles. The packaging cell line competiess a mammallan cell, a retroviral DNA competies and lentry russ, preferably HIV, appol, where the coding sequence for a lentrivirus, preferably HIV, appol, where the coding sequence has been mutagenised to improve expression of the viral gappol proteins, a second retroviral nucleotide sequence.
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                                sequence is a common region found in Gay coding sequences: Gay protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy or gene replacement with improved safety. They can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               third retrovital nucleotide sequence comprising a DNA sequence of interest and lentivirus, preterably HIV, cis-acting sequences required for packaging, reverse transcription and integration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV: dat: packaqing cell line; lentivirus; retroviral vector particle;
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                        1 damatraaggaaggemeeaaggaageetteegegactaegtggacegettetteaagaee 60
intection and acquired immunodeficiency syndrome (ADS). The present
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independent BiV derived refroviral vector particles, useful in gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy; gene replacement; waccine; biochemical reagent;
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                                                                                                                                                                                                                                    89.3%; Score 53.6; DH 21; Length 1268;
93.3%; Pred. No. 2.2e-08;
                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                   Sequence 1268 BP: 273 A; 449 C; 411 G; 135 T; 0 other;
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0; Mismatches 4,
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/product="qag-profein"
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Matches 56; Conservative
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P-PSDR: AAY70599
                                                                   and cad polymerase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA252051;
                                                                                                                                                                                                                                                                                                    Matches
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333×88×8E

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qaapol sequence. This sequence is used in the packaging cell line. Codon optimisation results in improved expression of the gagpol protein and reduces the risk of recombination between the transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cassette, Gaq MedSP2. The Gay protein of HIV is needed for the assembly of virus-like particles, in addition, the Gay protein is involved in many stages of the HIV life evel, including assembly, virion maturation after particle release and early posternity steps in vioa replication. The expression cassette may be used for the recombinant expression of
in the development and production of vaccines and biochemical reagents. The present sequence is a gas coding region of codon optimised BIV
                                                                                                                                                                                                                                                                         HIV Gig-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                      1 gaeateaageagggeeeraaggageeetteeggaetaegtagaeeggttetteaagaee 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expression cassettes eneroding the baman immunedatiology virus (HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the coding sequence of a HIV day expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic HIV Gag expression cassette coding sequence Gag.ModSF2.
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                                                                                                                                                                               89.3%; Score 53.6; DB 21; Length 1503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      containing polypeptide useful for vaccinating against BIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Zur Megede J, Srivastava I, Lian Y, Harted K.
Selby M, Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infections and acquired immunodeficiency syndrome (Albs)
                                                                                                                            Sequence 1503 BP; 339 A; 530 C; 433 C; 201 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1515 BP; 329 A; 547 C; 480 G; 159 L; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV-1; AIDS; Gag; vaccine; expression cassette; ss.
                                                                                                                                                                                                                  4
                                                                                                                                                                                                   Pred. No. 2.2e-08;
                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                  AAA70412 standard; DNA; 1515 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Fig 7; 391pp; English.
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                                                                                                                                                                                                   93.38;
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Best Local Similarity 94.34
Matches 56, Conservative
                                                                                                                                                                                                                  56; Conservative
                                                                                           vector and gagpol mRNA.
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                                                                                                                                                                                                   Similarity
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Greer C, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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(CHIR ) CHIRON CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the coding sequence of a HIV Gaq-protease expression cassette, GagProt.ModS. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post cut; steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gaq-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS).
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                   862 ganateegeeagygeeeeaaggayeetteegegaetaegtgganngnttetaeaagaee 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expression cassettes encoding the human immunodeficiency virus (HIV) Gaq-containing polypeptide useful for vaccinating against \rm HIV infections and acquired immunodeficiency syndrome (AIDS) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                     HIV Gag-protease expression cassette coding sequence GagProf.ModS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hartog K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV-1; AIDS; Gag-protease; vaccine; expression cassette, ss.
                                                                                                                                                                                                                                                                                                                  HIV-1; AIDS; Gay-protease; vaccine, expression cassette, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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elby M, Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA70475 standard; DNA; 1865 BP
                                                                                                                                  AAA70413 standard; DNA; 1853 BP
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Best Local Similarity 93.3%
These 56, Conservative
                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  W02000 39 402-A2
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                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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                                                                                                                                                                               AAA70413;
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                                                                                          RESULT 11
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HIV Gag-protease expression cassette coding sequence GagProtMod.SF2(GP2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l gacatcaagcagggccccaaggagccttnngngactangtggaccgcttcttcaagacc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression cassettes encoding the human immunodeficiency virus (HIV) Gaq-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
                                                                                                                                                                                                                                                                                                                                                                                    Liu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.3%; Score 53.6; DB 21; Length 1865; 93.3%; Pred. No. 2 38-08;
                                                                                                                                                                                                                                                                                                                                                                         pede J, Srivastava I, Lian Y, Hartog K,
Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV-1; AIDS; Gag-protease; vaccine, expression cassette; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1865 BP, 424 A, 627 C, 583 C, 231 T, 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                          Zur Megede J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WP1; 2000-452400/39.
                                                                                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 Selby M,
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                                                                                 WO200039302-A2.
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                          Synthetic
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                                                                                                                                                                              The present sequence is the redied sequence of a BIV Cag-protease expension caserte. Sathrohad-SEZCED. The cag protein is needed for the assembly of vitus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a HTV Gaq/Hepatitis C virus (HCV) core tusion coding sequence. The Gag protein of HTV is needed for the assembly of
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 garatruagragggreeraaggageertteegegaartagagaettetteaagare 60
                                                                               Expression cassettes erooding the human immunodeticioney virus (HIV) dag containing polypeptide useful for vaccinating against HIV
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                                                                                                                                                                                                                                                                                                                                                                                               89.3%; Score 53.6; DB 21; Length 1865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gag containing polypeptide useful for vaccinating against HIV intections and acquired immunodeficiency syndrome (AIDS) -
     Marroy F.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                 intertions and acquired immunodeficiency syndrome (AIDS)
                                                                                                                                                                                                                                                                                                                                             Sequence 1865 BP; 460 A; 583 C; 569 G; 253 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV-1; AIDS; Gay; vaccine; expression cassette; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic HIV Gag/HCV core fusion coding sequence.
     Lian Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.3e-08;
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    Mismatches

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   Crivactava !
                                                                                                                                               claim 5; Fiq 70; 391pp; English.
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                  Selby M. Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus.
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Selby M, Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                13.83
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   Zur Megede J.
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                  WPI: 2000-452400/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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Barnett S.
Greer C. Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barnett S,
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                                                                                                                                                                                                                                                                                                               (AIDS)
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expression cassette, GaqPol.ModSF. The Gaq protein of HIV is needed for
the assembly of virus-like particles. In addition, the Gaq protein is
involved in many stages of the HIV life cycle, including assembly, virion
                                                                        present sequence was cloned and used to generate the expression cassettes of the prosent invocation. The expression eassettes may be used for the recombinant expression of HIV Gaq-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome
virus-like particles. In addition, the Gao protein is involved in many staces of the HIV life "yele, insteading assembly, virion maturation after particle release and early post-entry steps in viral replication. The present invention relates to synthetic HIV Gao expression cassettes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replication. The expression cassette may be used for the recombinant expression of HIV Sag polypoptides which may then be used to Faceinate against HIV intection and acquired immunodeficiency syndrome (AIDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     maturation after particle release and early post-entry steps in viral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV Gag-polymerase expression cassette coding sequence GagPol.ModSF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the coding sequence of a HIV Gag-polymerase
                                                                                                                                                                                                                                                    89.3%, Score 53.6, DB 21; Longth 2031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV-1; AIDS, Gag polymerase, vaccine, expression cassette, ss.
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                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                           Sequence 2031 BP; 421 A; 707 C; 646 G; 257 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Green C, Selby M, Walker C;
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                                                                                                                                                                                                                                                                      Pred. No. 2.3e-08;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                Query Match
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Score 53.6; DB 21; Length 4319; Fred. No. 2.5e-08;

89.3%; 93.3%;

Owery Match Best Local Similarity

0; 0; Caps 4; Indels 0; Mismatches Matches 56; Conservative

Oy Dp

Search completed. August. 8, 2001, 18:24:58 Job time: 12602 sec

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August 8, 2001, 14:54:56 ; Search time 5719-75 Seconds (without alignments) 162.256 Million cell updates/sec
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4b_ball;

4b_ind 1;

4b_ind 2;

4b_ov;

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4b_pall;
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TAMME	CONTRACTOR TO	

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	10	AF201927	AF202464	AF202465	AF287354	AF287352	AF287354	AX019132
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	Query Match Length DB 1D				1548			
œ	Query Matich	i		89.3	94·0	84.0	84.0	71.7
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Location/Qualifiers
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Human imm
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Selby,M., Otten,G.R. and Barnett,S.W.
Increased expression and immunoueulcity of sequence modified human
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A.1286509
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zur Megede, J. and Barnett, S.W.
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KEYWORDS
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RESULF
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/transl_table=11
/product "gaq-protease fusion protein GP1"
/product "gaq-protease fusion protein GP1"
/db_xret=for:7229425"
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VEEKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMUMIKETINDEAAABAWWH
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Lour Merdedo,J., Chen,M.C., Doe,B., Schaefer,M., Greer,C.E.,
Schby,M., Otten,G.R. and Barnett,S.W.
Increased expression and immunogenicity of sequence-modified human
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89.3%; Score 53.6; DB 56; Length 1847;

Query Match

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Fuller,M. and Anson,D.S.

    (bases 1 to 1548)
    Fuller, M. and Anson, D.S.

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RTRGAHTNDVKOLTEAVQKTATESTVIWGKTPKFKLPTQKETWETWITETWGATWIFFE
WEEVHTPLVKLWYQT PKEPTTGAFTPYVDGAANMETKI.GKAGYVTNKGPGKVVSI.TD
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DITAYDIQTKELOKQITKIQNFRVYYRDSRDPIJMKGPAKLLMKGEGAVVIQDNSDIKV
VPRPKAKITHDVGKQMAGDDCVAGRQDĒD"
                                                                                                                                                                                                                                          YSPTSTLDÍRQGPKEPFRDYVDRFYŘTÍRABOASÓBÝKNWMTRTTÍRONANPDCKT TL
KALEPAATLEFMMTAPPGPVSGPHKAFVLABAMSQVTNSATTMMGEGNFRNGRKTVKC
FNOGKBGHTAKNCKAPFKKGGWKOGKBSHQMKT*TFREANFLGKTMFSHFGFFGNFTG
SRPEPTAPSBESVRFGBETTTPSQKQEFIGKELYPLASLKSLFGSDFSSQ*
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PRSTKMPKLVDPPELNKPTQDEWEVQLATPHPAALKKKKSVIVLDVGDAYFSVPEHED
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TVQPIVLPEKDSWTVNDIQKLVGKLNMASQIYAG IKVRQLCKILRGTKALTEVIPLTB
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LPPVVAKELVASCDKCQLKGEAMHGQVINGSPGTWQLDCTHLEGKVTLVAVHVASGYTE
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                                                                                                                   /translation**MMARASVLSAGFI.RKWERIPIPPOARKGVPI.KHIVWASPFI.FPF
AVDPGLLETSEGGRQILGQLQPSLQTGSEELRSLYNTVATLYCVHOKIEVKDTKEALE
                                                                                                                                                                        K I EEEQNKSKKKAQQAAADTGNSSQVSQNY P I VQNLQGQMVHQA I SPRTENAWVKVVE
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GTGGET KVPQYPQTPIETCGHKATGTVLVGPTPVNTTGKNIL-FOTGCTLNFFISENIET
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                                                                                                                                                                                             EKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAEWDRLHPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      886 GACATCAGGGAGAGACCAGAGGAGGCTICAGGGATTAGGTGGACAGGTTCTACAAGAGC 945
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                                            /product="qag_protein"
/protein_id~"AAG28735.1"
/db_xref="G1.11066862"
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/protein_id="AAG28730.1"
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                          /transl_table=11
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TAVOMAVETHNPYPRGGTGGGYSAGERTVNTTATGTGTKELGKOTTKTONFRVYYRGSR
DELWGGFAKLLWRGGGAVVTONSGTRVVPPKRKTTFLYGRGMAGDGVAGROED"
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AVDPGLLETSER"PULDQUQPSLATGSFELPSLYNTVATLYCVHOKIEVKDIKEALE
KIEEEONKSKKKAQQAAADTGNSQVSONYPIVQNLQGQWVHQAISPRTLNAWVKVVE
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HAGPTAPGOMREPRGSDIAGTTSTLQEOIGWMTNNPPIPVGEIYKRWILLGLNKIVRM
YSPTSILDIRQGPKEPPRDYVDRFYKTI.RARQASQEVKNWMTETLLVUNANPDCKTIL
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CTEMEKEGKISKIGPENPYNTPVFAIRKKDSTKWPKLVDFFELNKFTQDFWEVQLGIP
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                                                      /note="derived from Human immunodeficiency virus type 1
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Viruses; Retroid viruses; Retroviridae; Lentiviius; Primate
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                                                                                                                                            /note="codon optimized reading frame"
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                                                                                                                                                                                                                           /product="gaq-pol fusion protein"
/protein_id~"AAC28737.1"
/db_xref="G1:11066865"
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/organism-"synthetic construct"
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/ordanism="synthetic construct"
/Ab_xrot-"taxon:12630"
/note:"qaqpoi-sequence"
/note:"qaqpoi-sequence"
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85.1%; Fitel. No. 0.00066;
71.7%; Score 43; DB 9; Langth 4307;
83.1%; Pred. No. 0.0066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.7%; Score 43; DB 9; Length 4307;
83.1%; Pred No 0.0066;
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Abyeret "taken 126.0"
Andre "Codon optimised quapol sequence"

    (bases 1 to 4307)
    Mitropharous, K., Kim, N.H., and Kotsopoulou, E.

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                                                                            0; Mismatches
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Patent: Wo 0055341-A 2 21-SPP 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2 from Patent WO0055341.
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    (bises 1 to 4307)
    don, M. and Mitrophanous, K.

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                                                                        Matches 49; Conservative
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                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTESSION
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Ab_xret "taxon: 426.30"
Ab_xret "taxon: 426.30"
Anote-"psFNKBP codom optimised HIV-1 gappol with leader sequence from the major splice donor"

1.58 < 1.58.2 q 700.1
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Pateut: Wo 0055441 A 14 21-SEP-2000;
UDEN MARK (GB) ; OXFORD BLOMEDICA LTD (GB) ; MITROPHAN-0GS KYRLACOS
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/dk_xrcf ""axon:326.30"
/note-"pSYNGP4 - codon optimised HIV-1 daupol with 20 bp
of the leader sequence of HIV-1, etc"
a 1194 c 1296 q 693 t
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Il gacateaageaqageco aaaqqaqoortto qeqartacqtqqaceqcttetteaaqae 59
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83.1%; Pred. No. 0.0066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-viral vectors
Patent: Wo 0055441-A 14 Z1-SEP 2000;
                                                                                                                                                                                                                                                                                                          Sequence 14 from Patent W00055341.
AX035465
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Uden,M. and Mitrophanous,K.
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Matches 49; Conservative
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/translation="QNIQOMVYQATSPRTINAWVKVIEEKAFSPEVIPMFSALAEKA
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/protein_id="AAF01901.1"
/db_xref="G1:6019103"
            /protein_id="CAB85850.1"
/db_xref="G1:7414162"
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/country "Tanzania"
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/product.="P24"
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Best Local Similarity 78.0%;
Matches 46, Conservative
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Matches 47; Conservative
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Submitted (27 OCT-1999) Peeters M., Retrovirus, Ird, BP 5045, 34032
Montpellier cedex 1, FRANCE
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paract we observed A 12 21 SEP-2000;
UDEN MARK (GB): OXPORD BIOMEDICA LID (GB): MITKUPHANGUS KTRIAGUS
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/note="pSYNGP2 - codon optimised HIV-1 gagpol with leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haman immuned-elected virus type 1 proviral partial gag gene for P24, isolate 97SE-1189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toure Kane, C., Montavon, C., Faye, M.A., Gueye, P.M., Sow, P.S., Toure Kane, C., Montavon, C., Faye, M.A., Gueye, P.M., Sow, P.S., Ndoye, I., Gaye-Diallo, A., Delaporte, E., Peeters, M. and Mboup, S. Identification of all HIV type I group M subtypes in Senegal, a country with low and stable serroprevalence AIDS Res. Hum. Retreviruses 16 (6), k04 609 (2000)
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Human immunodeficiency virus type 1.
Viruses, Retroid viruses, Retroviridae, Lentivilus, Frimate
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83.18; Pred. No. 0.0065,
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AX035463
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/country="Senegal"
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/trānslation="kivrmyspvslldirdgereperdyvdrefktlrargatodykn
wmfetllivonnupdcknilkalgegatleemmtacggvggpshkarvlabamsganna
nvmmgrgnfkgprrikcfriggegghlar"
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TPODI.NTMINTVGGHQAAMQILKDTINEEAAEWDRLHPVHAGPVAPGQIREPRGSDIA
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| Punjife, F. (libert. P., Chaplin, B., Vannberg, F., Mwakagile, D., Msananga, G., Hunter, D., Fawzi, W. and Essex, M.
| Emerging recombinant human immunodelicieucy viruses: uneven representation of the envelope V3 region Albs 13 (13), 1613-1621 (1999)
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Human immunodoficiency virus type 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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Pred. No. 0.28;
O; Mismatches 13; Indels 0:
                                                                                                                                                                                                                                                    65.3%; Score 39.2; DB 59; Length 663; 78.3%; Pred. No. 0.13;
Live 0; Mismatches 13; Indels 0;
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Heyndrickv, E., Tanssens, W., Zekeng, L., Musenda, E., Anagonou, S., Van
der Auwerd, G., Coppens, S., Voreecken, K., De Witte, K., Van
Rampelbergh, E., Kahindo, M., Morison, L., Meditchan, F.E., Carr, J.K.,
Albert, J., Essex, M., Goudsmit, J., Asjo, B., Salminen, M., Buve, A.,
Study Group on Heterogeneity of HIV Epidemics in African Cities and
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Submitted (08-SEP-1999) Virology Unit, Dept. of Microbiology,
Institute of Tropical Medicine, Nationalestraat 155, Autwerpen,
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J. Virol, 74 (1), 363-370 (2000)
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BR356040 DG1_121_H
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1 (bases 1 to 491)
                                                            AA143927
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Match Length DB - ID
                                                                                                                                     oryza sativa
                                Score
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                                       28.4
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BGS17417 569 bp mRNA EST (0-MAK-2001) 947062612.y) 947 · 2 week about from barkan lab Zea mays cDNA, mRNA sequence.
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Site 1: Except; Site_2: Khof; Directionally cloned using
State agenc's Unizap Kr cDNA cloning kit with the 5' end
at the Erok! site, The library represents 8 x 10e5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /ordanism="orgza sativa"
/strain="Nipponbare"
/strain="Nipponbare"
/cle.re: "151244_22"
/clone_lib="Rice cDNA from immature leaf including apical meristem"
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clade, Panicoideae, Andropogoneae, Zea.
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Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
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/tissue_type "leaf and stem, including leaf base"
/dev_stage "2 week old seedling (* leaves)"
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Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
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Tel: 650 723 2227
Fax: 650 725 8221
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Plate: 947062 row: C column: 12.
Location/Qualifiers
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Stanford University
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                                                                                                                                                                                                                                                                                                                                                       Email, tsasakidabr.atfrc.go.jp
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Tel: 0298-38-7441
Fax: 0298-38-7468
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/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryola, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida, Foales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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   independent recombinant phage. The plants were greenhouse
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/dev_stage="adult"
/lab_host="DH108"
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DEFINITION FM1_53_H06.91_A003 Floral-Induced Meristem 1 (FM1) Sorghum
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855 California Ave, Palo Alto, CA 94304, USA
                                                                                                               Query Match 47.3%; Score 28.4; DB 154;
Best Local Similarity 70.4%; Pred. No. 34;
Matches 38; Conservative 0; Mismatches 16;
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68.4%; Pred. No. 39;
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Email: walbotestanford.edu
Plate: 707011 row. F column. 07.
Location/Qualifiers
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AW147097
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Elkaryola, Viriliplantan, Stroptophyta Pmbryophyta; Tracheophyta;
Spennatophyta, Manollophyta, Liliopsida; Poates; Poateer; PNCC
clade; Panicoldeae, Andropogonoae, Eca.
1 (bases 1 to 216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mmpratt@uga.edu
Seguenkes have been trimmed to explude PelyA, vector and regions
below phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                            Eukaryoti, Viridiplintae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Maquoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                            Cordonnier-Pratt, M - M., Gingle, A., Sudman, M., Marsala, C. and Pratt
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Flant Sciences Building, Em. 2502, Athens, GA 30602-7271, USA
Flant 706 542 1860
Fax: 706 542 1805
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An EST database from Sorghum: floral-induced meristems
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Aa143927
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High quality sequence stop: 141
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Department of Botany
BG050418.1 GI:12503099
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EST.
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                                                                                                                                                                                                                                                                                 /clonc_lib "Maize Leat, Stratagene #937005"
/moto="Vector Uni-YAP: Site_l-FcoPl: Site_2: Xhol: mENA
isolated from illuminated leaves and sheaths of 5 week old
plant: cDNA directionally cloned into vector. "
is 6: c 55 g 49 t.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eubergeta: Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsidu; Podies; Póaceae, PACC
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | NESS6640 | 219 bp | mRNA | EST | 20-JUL 2000 | DAL-L2L_H05-91_A002 Dark Grown | (DG1) Sorghum bicolor CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The University of Georgia
Plant Sefences Building, Pm. 2502, Athens, GA 30602-7271, USA
Pax: 706-542-1805
Pax: 706-542-1805
                                         Dept Biol Sci, California State Univ, Hayward, CA 94542
Tel: 5108853459
                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.7%; Score 28; DB 2; Lengtl 216, 66.7%; Pred. No. 40; tive 0; Mismatches 20; Indels
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/elone_lib="bark Grown 1 (DG1)"
                                                                                                          Email: cbaysdor@haywire.esuhayward.edu
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High quality sequence stop: 219
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Zorganism "Zea mays"
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Department of Botany
                       California State University
                                                                                                                                                                                                                                                                 /clone="csuh00762"
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                                                                                                                                                                                                                     /strain-"B73"
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Contact: Baysdorter C
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Best Local Similarity 66.7%
Merches 40; Conservative
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                                                            Tel: 5108853459
Fax: 5108854747
                                                                                                                               Seq primer: SK.
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from 8 week old plants; Vector: pHinoscript II from Lambda Zap II; Site_1: Xhol; Site_2: Bookl; The library was made from pair A FNA in the clearable weeter I umbda ZaP II.
Clones to be sequenced were prepared by mass excision."
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 327)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
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//db_xr=="taxon:4558"
//clonc_lib-"Ovary ! (UVI)"
//note="Organ: Mix_of ovaries of varying immature stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,L.H.
An EST database from Sorghum: cvaries of varying immature stages
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                                                                                                                                            0; Gaps
                                                                                                                    1 gacatcaagcagagccccaaqgagccittergcgactacqtygaccqcttrttcaagarc 60
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The University of Georgia
Flant Sciences Building, Em. 2502, Athens, GA 80602 7271, USA
Tel: 706-542-1805
Fax: 706-542-1805
                                                                                                                                                                                                                                                                                                                  21 - NOV - 2000
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     46.7%; Score 28; 3B 166; Lonath 219;
66.7%; Pred. No. 40;
tive 0; Mismatches 20; Indels (
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High quality sequence stop: 266
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Contact: Cordonnier-Pratt MM
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                                                                40; Conservative
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Query Match
Best Local Similarity
Matches 40; Conserva
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae,
Ehrhartoideae, Oryzcae, Oryza.
1 (bases 1 to 347)
                                              Eukaryóta, Vinidipiantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales; Poaceae, PACC
clade; Panicoideae; Andropogoneae; Zea.
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AUG97510 Rice shoot Oryza sativa cDNA clone S5505, mRNA sequence.
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/clone_llb="48b - leaf primordia cDNA libiary from Hake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="leaf primordia"
/dev_stage="P7-F11 leaf"
/dev_brot="E.coli XLI-Blue MFR'"
/norpam: shoot: Vector: Lambda zap: Hake lab cDNA
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Contact: Takuji Sasaki
National Institute of Agrobiological Resources
                                                                                                                                                                                                                                                           855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2327
Fax: 650 725 8221
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Rice cDNA from etiolated shoot (2000)
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Plate: 486049 row: D column: 10.
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PROJECT ='RGP'
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91 c
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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AU029576 Kice panicle shorter than 3cm Oryza sativa cDNA clone
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DEFINITION C99276 From Famicle at ripering stage Oryza sativa CDNA clone
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            /strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
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/note="Etiolated shoot (8 days old)"
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/ncte="@rgan: paniele"
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/orqanism="Oryza sativa"
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/db_xref="taxon:4530"
/clone="E31104_62"
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Rice CDNA from panicle
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                                               /rlone="S5505"
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                                                                                        Enkaryota: Viridiplantae: Stroptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Maqnoliophyta; Liliopsida; Poales; Poaceae;
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[ Chases 1 to 364]
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Plant Sciences Building, Rm. 2502, Athems, GA 30602-7271, USA
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/dev_stage "ripening stage"
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National Institute of Agrobiological Resources
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               C99276.1 GI: 4762028
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KEYWORDS
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                                                                                                                                                KELEKEN,E
                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                     JOURNAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
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/clone_lib "Gwary 1 (OVI)"
/hote="Organ: Mix of evaries of varying immature states
from 8-week-old plants: Vector: pHluescript II from Lambda
                                                                                                                                                                                                                                                                                                Zap II: Site_I: XhoI: Site_2: BrokI: The library was made time poly A RMA is the closing vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

1 107 c = 103 g = 88 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION 05c04f07-121 membrane-tree polysomes from endosperm Zea mays cONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, I., Helentjaris, I., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dept. of Plant Sciences, University of Arizona, Tueson, AZ,85721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta, Magnellophyta, Lillopsidu, Podles, Poaceae, PACC
elade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; daps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gadat daagddagggeeddaaggageet filtinegegad ang tiggaandget fiet finaagaeer 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 - OCT - 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Partial sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 46.7%; Score 28; DB 141; Length 464;
Local Similarity 66.7%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Biological Sciences, School of Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interdisciplinary Center for Biotechnology Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone 05c04107 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Mol. Biol. 26, 1085-1101 (1994)
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                                                                                                                                                          /organism-"Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E-mail: helnjars*ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helentjaris TG (primary contact)
                          High quality sequence start: 8
High quality sequence stop: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: The Maize con Project
                                                                                                                                                                                       "taxon.4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mEMA
                                                                                                        Location/Qualifiers
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ph: 904-392-1928, ext. 301
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University of Florida
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Seq primer: PolyTMix
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ph: 510-881-3459
                                                                                                                                                                                       /db_xret
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/note="Wector: ZipLox, Site]: Sall; Site_2: Not1; ds-cUNA was prepared from oligo-dT selected mRNA by priming with a Not1 oligo-dT oligomer and then adding the Second Strand to RNase nicked DNA:RNA hybrid with DNA Poll. Sall adaptors were added to the ends, the ds-cDNAs were then digested with Not1 and size-selected. These were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             directionally-cloned into the ZipLox phage vector, excised as plasmids, and then individually analyzed. # 98 c 107 g 68 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Sorghum bicolor"
/db xref="taxon:458"
/db xref="taxon:458"
/clone_lip-"Fetbloogu induced 1 (PII)"
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
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ptl_54_gn6 gl_A002 Pathogen indured 1 (Pfl) Sorghum bicolor cDNA,
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Science's Building, Rm. 2502, Athens, GA 10602-7271, USA Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="membrane-free polysomes from endosperm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.7%; Score 28; DH 188; Lenyth 364; 66.7%; Pred. No. 43; tive 0; Mismatches 20; Indels 0
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                                            E-mail: robferl@nervm nordc ufl edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence start: 112
High quality sequence stop: 329
                                                                                                                                                                                                                                                                                          /db_xref="taxon:4577"
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Contact: Cordonnier-Pratt MM
Department of Botany
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                                                                                                                                                                                                      /organism="%ea mays"
/strain="W64A2"
                                                                                        Seq primer: F21.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                          /clone="05c04f07"
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fax: 904-392-4072
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Best Local Similarity
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BE595775
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from 8-week-old plants; Vector: pBiteScript II from Lambda 2ap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the clouding vector lambda 2AP II. from s. to be sequenced were prepared by mass excision.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukāryota; Viridiplantac, Streptophyta, Emkrysphyta; Tranhonphyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 371)
                                                                                                                                                                                                                                                                                                                                                                                              sequenced were prepared by mass excision waRNING: While most or all ESTs are expected to derive from the host plant, or effort was made to climinate ESIs deriving from the pathogen."
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cultivar) were infected with pathogen (isolate FRM421 of Colletctrichum graminicola, which is a sorghum isolate). Who was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptibit; to anthrachose disease. The library was made from poly-A RM in the cloning vector lambda ZAP II. Clones to be
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/note="Organ: Mix of ovaries of varying immature stages hote="Organ: Mix of ovaries of varying immature stages and the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the stages of the s
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Plant Schemes Building, Rm. 2502, Athens, GA 30602-7271, USA
Plant Schemes Building, Rm. 4502, Athens, GA 30602-7271, USA
Fax: 706 542 1805
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Contact: Cordonnier-Pratt MM
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Spermatophyta; Magnoliophyta; Filiopsida; Poalos; Poacosa; PACC
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9420510.91 947 - 2 wood shost from Barkan Lib Zeu mays CDNA, mKNA
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Walbot, V.
Walbot, V.
Walso ESTs from various cDNA libraries sequenced at Stanford
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/tissue_ype="total and stem, including real base"
/dev_stage="Z week old seedling (3 leaves)"
/lab_nost "XLI-Hlue"
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Hest Local Similarity 70.4%; Prod. No. 44;
Matches 38; Conservative 0; Mismatches 16; Endels 0;
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Stanford University
855 California Ave. Palo Alto, CA 94404, USA
Pax: 650 724 2221
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Tel: 650 723 2227
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Plate: 947061 row: G column: 10.
Localion/Qualifiers
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                                                                                                                                                        Dhail. walbotestanlord.edu
Plate: 947073 row: D. column: OB
Location/Qualifiers
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/oultivar "B73"
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Contact: Walbot V
Contact: Walbot V
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947074H04.y3 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA
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Spermatophyta; Magnoliophyta; Liliopsida, Poales; Poaceae, FACC
clade; Panicoideae; Andropoyoneae; Zea.
1 (bases 1 to 592)
              Stratagene's Unizap_XR cDNA cloning kit with the 5' end at the EcoRI site. The library represents 8 x 10c5 independent recombinant phage. The plants were greenhouse
Site_1. ErrRI; Site_2. XhrI; Directionally cloned using
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Maize ESTs from various cDNA libraries sequenced at Stanford
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/clone_lib="947 - 2 week shoot from Barkan lab"
/tissue_type="lag" and stem, including leaf base"
/dev.stage="2 week old seedling (3 leaves)"
/lab_host="XLI-Blue"
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Fax: 650 728 8221
Email: walbot@stanford.edu
Plate: 947074 row: B column: 04.
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/cultivar="B73"
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Best Local Similarity 70.4%
Matches 38; Conservative
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Contact, Walbot V
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RESULT

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Triticum aestivum
Eskaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida, Poales; Poaceae; Pooldeae
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Minnow, E. Andorschi, U.D., Chao, S., Phin, A., Choi, D. W., Close, T.J.,
Dyorak, J., Fenton, R.D., Ban, P.S., Hsia, C.C., Kang, Y., Kianian, P.,
Lazo, G.R., Miller, R., Otto, C., Navyen H. T., Pansch, C.J., Shafon
C.L., Simons K., Tong, J.C. and Zhang, D.
The structure and tunction of the expressed portion of the wheat
genomes - Salt-stressed sheath CDNA library
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WHE2066_BG7_D142S Wheat salt stressed sheath cDNA library Triticum
acstirum cDNA clone WHE2065_B07_D14, mPNA sequence.
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
olade, Fanicoideae, Andrepogoneae, ?oa
1 (bases 1 to 585)
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   AW147097 585 bp mRNA EST 03-NOV-1072 7070]
Hydr Mixed adult tissues from Walbot lab (SK) Zea
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03-NOV-1999
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855 California_Ave. Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Walbot V
Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Zea mays"
/cultitar="W23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel. 650 723 2227
Fax: 650 725 8221
Email: walbort@stanford edu
Plate: 707011 rrw F column
Location/Qualifiers
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221 c 282 a
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/lab_host="DH108"
                                                 mays cDNA, mRNA sequence. AW147097
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                                                                                                                      AW147097 1 CI-6194993
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                                               US bepartment of Africulture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Horhanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at the University of California, Riverside (Akhanev, Chin
Choi. Close, Penton. Kianian, Otto. Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the Ob Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Busearch Center West Area, Western Regional Busearch Center Technology Street, Albany, CA 94710, USA 10559577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukıryılı; Viridiplantur; Streptophyta; Embryophyta; Trachecphyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ancto. "Vector: Lambda Uni-ZAP XK, excised phagemid; Sire.": EcoRI Sile.: Xhol; Plants Were grown under hydroponic conditions at UC havis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in J Dworak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library was made, and the COMA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="WHE2066_BO7_D14"
/clone_lib="Wheat sail=stressed sheath cDNA_library"
/fissue_type="Sheath"
/dev_stage="Adult plant"
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                                                                                                                                                                                                         Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.7%; Score 28; DB-152; Length 524;
66.7%; Pred. No. 58;
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Zdb_xref-"Laxon-4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host "E. coli Sulk"
                                                                                                                                                                                                                                                              Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                        Email: oandersnapw.usda.gev
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1 (bases 1 to 647)
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Fax: 5105595818

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Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Riverside, Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson Tab (all other authors and DNA sequencing were performed in the OD Anderson Dab (all other authors and DNA).
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BESST_15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                total RNA and poly(A) BNA were prepared, a chNA library was made, and the CBNA clones were in vivo excised to give pBluescript phagemids in the LJ Close lab (Choi,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Site_1: FcgRI; Site_2: XhoT; Plants were grown in the greenhouse. Spikes at 5, 10 and 15 DAP were harvested,
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Cordonnier-Pratt,M.-M., Gingle,A., Dean,R., Sudman,M. and Pratt
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Plant Sciences Building, Bm. 2502, Athons, GA 30602-7271, USA
                     Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 seq primer. Stratagene SK primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Close, Fenton) at the University of California,
                                                                                                                                                                                                  /cultivar-"Chinese Spring"
/db_xxel-"taxou:4565"
/clone "MIR0926_B11_122"
/clone_lib "Wheat 5-15 DAP spike cDNA_library"
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66.7%; Pred. No. 59;
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/dev_stage="Adult_plant"
/lab_host-"E. coli_sol.R"
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Email: oandersnapw.usda.gov
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Query Match
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                                                                                                                                                                                                                                                                           grow older (4 weeks or older), plants resume susceptiblity to authrachose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be
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Spermatophyta, Magnoliophyta; Liliopsida, Podles, Poaceae; PACC
clade; Panicoideae, Andropogoneae; Zea.
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                                                                                                                  cultivar) were infected with pathogen (isolate FRM121 of colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they
                     /note="Organ: Anthracnose-infected leaves from two-week-old sorghum plants 48 hr after inoculation; Vector: pBluescript II from Lambda Zap II: Site_1. XhoI. Site_2: EcoRI; Two-week-old southum plants (BTX 623)
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/tissue_type="leaf and stem, including leaf base"
/dev_stage="2 week old seedling (3 leaves)"
/lab_host="XL1-Blue"
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Best Local Similarity 69.8%; Pred. No. 87;
Matches 37; Conservative 0; Mismatches 16; Indels 0;
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/clone_lib="Pathogen induced 1 (Pil)"
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855 California Ave, Palo Alto, CA 94304, USA
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/cultivar="B73"
/db_xref="Laxon:4577"
/clone_lib="947 - 2 we
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Location/Qualifiers
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Contact: Walbot V
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Spermatophyta, Magnollophyta, Elliopsida, Poales, Poaceae, PACC
clade, Panicoideae, Andropogoneae, Sorghum.
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//db_xref="tuxon:4558"
/clone_lib==bathogen induced 1 (Pil)"
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
/vorce*-Ord sorghum plants 48 hr after incoulation:
/vorcer: pBluescript II trom Lambda Zap II; Site_1: XhoI:
site_1: EcoPI: Two-week-old sorghum plants (BTX 523)
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Sequences have been trimmed to exclude PolyA, vector and regions
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Plant Sciences Building, Rm. 2502, Athens, GA 30502-7271, USA
TPI: 706 542 1860
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Pred. No. 88;
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69.8%; Pred. No. 87;
tive 0; Mismatches
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Matches 37; Conservative (
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Permitophyta: Mardolisphyta: Liliopsida: Poales: Poaceae; PACP
clade: Panicoldese: Acdropogeneie; Zea.

    (bases 1 to 408)

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade: Funicoideae; Andropogoneae; Zea.
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69.8%; Prod. No. 88;
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855 California Ave, Palo Alto, CA 94304, USA
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Location/Qualifiers
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Fax: 650 725 8221
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Stratagenes's Buizap XK cDMA clouing Kit with the 5' end
at the Ecokl site, The library represents 8 x 10e5
independent recombinant phage. The plants were greenhouse
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Stantord University
855 California Ave, Palo Alto, CA 94404, USA
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Fax: 650 725 8221
Email: walbot stanford, edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
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BG316823 470 bp mFNA EST z_0 FEB z_001 947027C02.x1 947 - 2 week shoot from Burkan lab 2ca mays cDNA, mENA
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Bukaryota, Vizidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermateghyta; Magnollephyta; Lilinepsida; Prales; Foaceae, FACC
clade; Panicoldege; Andropogoneae, Zea.
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                                                                                                                                                                                                                                               Eukarýóta, Viridipiantae, Streptophyta, Embryophyta, Trawhenphyta, Spermatophyta, Magnollophyta, Liliopsida, Foales, Poaceae; PATC clade, Pantooldeae, Andropwwoneáe, Sea.
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Tab Zea mays cDNA, mRNA sequence.
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/clone_lib="947 - 2 week shoot from Barkan lab"
/tissue_type="tag" and stem, including leaf base"
/dv_stage="z week old seedling (3 leaves)"
/lab_host="XL1-Blue"
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tive 0; Mismatches 15; Indels 0;
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Fax: 650 725 8221
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plate: 947027 row. C column
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SUMMARIES

	Description	HIV Gaq major homo	HIV synthetic Gaq	HIV codon-optimize	HIV p55 Gad Major	BIV Gag common reg	Codon optimised Hu	Synthetic HIV Gag	HIV Gag-profease e	HIV Gad-protease e	HIV Gag-protease e	Synthetic HIV Gag/
	9	AAA51608	AAA51610	AAA51626	AAA70426	AAA70417	AA252051	AAA70412	AAA70413	AAA70475	AAA70476	AAA70415
	¥.	6.0 21	2.1	2.1	 	7	21	2.1	<u>.</u>	2.1	7	74
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HIV Gag polymerase	HIV biristronic co	MIV bicistronic co	HIV bicistronic co	MIV bicistronic co	Packaging construc	HIV Gad major homo	HIV synthetic Gad	HIV codon-optimize	HIV dadpol SYNdp	Human immusodetic	Nucleotide sequence	HIV partial leader	HIV partial leader	HIV complete leade	Bumanised BIV-1 da	Synthetic HIV gag	Humanised HIV-1 da	Attenuated HIV-1	BIV-1 non-subtyper	HIV I non subtype	Major homology red	Sequence of a ribo	Sequence of day de	Sequence of a ribo	Sequence of a ribo	BIV-1 dad qene.	HIV-1 dad gene.	Sequence of a ribe	Separate to Separate of a ribo	Stringer Company	Chimeric chemokine	Chimerie chemekine	
AAA70414	AAA70472	AAA70474	AAA70471	AAA70470	AA252055	AAA51607	AAA51609	AAA51625	AA208740	AAA93972	AAC85876	AAA9 : 984	AAA93983	AAA94982	AAF 11286	AAV45173	AAF31283	AA114180	AAP57929	AAP57926	AAA51627	AAN92332	AAN70258	AAN92433	AAN92334	AAQ80573	AAT33293	AAN92346	AAN 92 3 45	11/1 1-11/11	AAC84863	AA134862	
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17.3	97.3	97.3	97.3	47.3	97.3	92.0	5. G.	9.7.0		7.9.7	7.1.7	1.6.7	74.7	74.7	78.7	78.7	1.	63.7	5. H. 3	£.3	57. 4	55.7	6.00	55.7	6.5.7	55.7	55.7	55.7	6.6.7	- :-		6.00	
58.4	58.4	4.80	58.4	58.4	58.4	55.2	C1 (S1)	55.2	6	47.8	47.8	17.8	47.8	47.8	47.2	47.2	47.0	18.2	35	u) e	34.4	33.4	33.4	13.4	43.4	13.4	33.4	3.3.4	43.4	7.3	÷. c.	4.5.4	
1.2	1 3	14	15	91 <	17	18	19	^ર 7		a	er er	ĉi	25	26	5.7	28	6.4 C4	3.0	3.1	C)	33	34	35	36	17	38	68	40		17	1.5	44	

ALLGNMENTS

AAA51608 standard; DNA; 60 BP (first entry) 31-0XT-2000 AAA51608; AAA51608 PFSULT

HIV day major homology region nuclectides 841-9400

Gag, expression cassette, antiquaic, type C. HIV, Env. synthetic; DNA immunication; packaging cell line; antique presentation; ss.

Human immunodeficiency virus.

W0200039304-A2,

06-JIII.-2000.

99WO-US 31273. 30-DEC-1999;

980S-0114495. 9908-0152195, 31-DEC-1998; 01-SEP-1999;

(CHIR) CHIRON CORP.

Barnett S, Zur Megede J;

WP1; 2000-452401/39.

Polymucheotide encoding antigenic type C HIV dag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV

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Gaps

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production of dag- and/or Envicontaining proteins. Synthetic Env and Gag explession cassettes exhibit increased potency for induction of cytotoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antique entlapped or associated to the immune system of the host.
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                                                                                               Expression cassettes comprising a polynucleutide encoding antigenic
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    100.0%, Score 60; DB 21; Length 1509; 100.0%; Pred. No 9e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type C strain AF110967.
                                                                                                                                                                                                                                                                                                                                                                                                               HIV codon-optimized synthetic Gag polynucleotide.
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                                                     0; Mismatches
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                                                                                                                                                                                                                                                                        AAA51626 standard; DNA; 1509 BP.
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                                                             hu; Conservative
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                                                                                                         production of Gay- and/or Envicontaining proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of cytocoxic T-lymphocyte (CTL) responses by DNA immunisation. Gag of HIV-1 self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antigen entrapped or associated to the immune system of the host.
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                                         Expression cassettes comprising a polynucleotide encoding autigenic type of human immunodeficeency virus (HIV) Gay of Env polyneptides are useful in DNA immunitation, generation of packaging cell lines and
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DNA immunization; packaying cell line; antigen presentation, SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 60; DB 21; Length 60; 100.0%; Pred No. 7 20:10;
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                                                                                                                                                                                                                                                                                Sequence 60 BP; 12 A; 24 C; 15 G; 9 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV synthetic Gag polynurleotide.
Claim 1: Page 92; 113pp; English
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Best Local Similarity 100 0
Matches 60, Conservative
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06-JUI,-2000

Synthetic

AAA51610;

AAA51610

Barnett S,

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WG200015819-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to synthetic HIV Gaq expression cassettes. The dat protein of HIV is needed for the assembly of TTTS like particles. In addition, the Gaq protein is involved in many stages of the HIV like cycle, including assembly, virion maturation after particle cassette may be used to the stages in whem replication. The expression cassette may be used for the recombinant expression of HIV Gattpolypeptides which may then be used to varcinate against HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infortion and acquired immunodeficiency syndrome (AIDS). The present sequence is the coding sequence of HIV p55 Gag Major Homology Region. This sequence is located Within the p24-CA sequence of Gag. Mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product "HIV p55 dag Major Homology Region protein"
/note≔ "No stop codon giveu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Zur Megede J. Srivastava I. Lian Y. Hartog K. Liu H. Selby M. Walker C.
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08.3%; Prod. No. 2.2c-09;
Live 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this region can severely impair particle production.
                                                                                                                                                                                                        HIV:1; AlbS: Gaq: vaccine; expression cassette; ss.
                                                                                                                                 HIV p55 dat Major Homology Region coding sequence.
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                                                                                                                                                                                                                                                                          Human immunodeliciency virus type l.
                                                                                                                                                                                                                                                                                                                                                     Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1: Page 345; 491pp; English.
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Best Local Similarity 98.3%
Marches 59, Conservative
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AAA70426.
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The present invention relates to synthetic HIV day expression cassettes. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post entry steps in viral replication, the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cassette may be used for the recombinant expression of HIV Gaq-polypeptides which may then be used to vaccinate against HIV interestion and a quinch image then be used to vaccinate against HIV sequence is a reminerabilities of syndrome (AHE). The present sequence is a common region found in Gaq coding sequences. Gaq protease and Gaq-polymerase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ] quealcequeaqqueet aaspasto the separtacity and quae quitetteaqqaet 60 HIIIHHHHHHHHHHHHHHHHHHHHHHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barnett S. Zur Megede J. Srivastava I. Lian Y. Bartoq K. Liu H.
Greer C. Selby M. Walker C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Codon optimised Human immunodeficiency virus gas coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92, 98, 375 v.C. FW 41, 196 22, Toropti, 12683, 98, 38, Pred. Bb, 2,7c-09;
Live 6, Mismarthes 1, Indexs 0;
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HIV-1; AIDS: Gag: varrine; expression cassette; ss
                                                                    Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 343; 491pp; English.
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Matches 59, Conservative
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/product-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON CORP.
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                                                                                                                                                WO200039302-A2.
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31-DEC-1998;
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                      01-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell line. Codon optimisation results in improved expression of the gaspol protein and reduces the risk of recombination between the transfer
                                                                                                                                                                                                                                                                                                                                       comprising the coding sequence for a heterologous envelope protein and a third retroviral purjectide sequence comprising a DNA sequence of interest and lentivirus, preferally HIV, cis-acting sequences required
                                                                                                                                                                                                                                                                                                                                                                   interest and lentivirus, preferably HIV. cis-acting sequences required for packaging, reverse transcription and integration. The packaging rell lines and viral particles can be used for gene therapy or gene replacement with improved safety. They can also be used in the development and production of varcines and hinchemical reagents. The present sequence is a gag coding region of codon optimised HIV gagpol sequence. This sequence is used in the packaging
                                                                                                                                                                                                                                                        The patent discloses new packaging cell line for producing a viral accessory protein independent lentivirus, preferably human immunodeficiency virus (HIV), denived retroviral vector particles. The packaging cell line comprises a mammalian cell, a retroviral DNA comprising a coding sequence for a lentivirus, preferably HIV, adapol, where the coding sequence for a lentivirus, preferably HIV, adapol, the viral gagpol proteins, a second retroviral nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gacatecgecagggeeeeaaggaceetteegegactaegtggaeegettetteaagaee 60
                                                                                                                                                                               New packaging cell line for producing a viral accessory protein independent HIV derived retroviral vector particles, useful in gene therapy or gone replacement.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 1503 BP, 339 A, 530 C, 433 G; 201 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV-1; AIDS; Gag; vaccine; expression cassette; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
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                                                                         98US-0100063. 6C
                                                            98US-0100022. 60
                                                                                                 (CHIL-) CHILDRENS MEDICAL CENT.
                                                                                                                                                                                                                                     Claim 41; Fig 8; 62pp; English.
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                                     99W0-US20675.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vector and gagpol mRNA.
                                                                                                                         Mulligan RC;
                                                                                                                                                 2000-271455/23.
                                                                                                                                                              P-PSDB; AAY70599.
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                                        10-SEP-1999;
                                                              11-SEP-1998:
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               23-MAR-2000
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                                                                                                                            Gray JT,
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The present sequence is the coding sequence of a HIV Gag expression cassette, Gag-ModSF2. The Gag protein of HIV is needed for the assembly of virus-like particles, in addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and carly post-entry steps in viral replication. HIV Gag-Pallyperides which may be used for the recombinant expression of HIV Gag-Pallyperides which may then be used to vaccinate against HIV infection and acquired immunodeliciency syndrome (AlDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expression cassettes encoding the human immunodelicioncy virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                        Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypoptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
                                                                                                                                    Barnett S, Zur Meyede J, Srivdstava L, Lian Y, Hartog K, Liu H;
Greer C, Selby M, Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV Gag-protease expression cassette coding sequence GagProt ModS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1515 BP: 329 A; 547 C; 480 G; 159 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA70413 standard; DNA; 1853 BP
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 7; 391pp, English.
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98US-0114495.
                             99US-0168471.
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Rest Local Similarity 98.39
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR ) CHIRON CORP.
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                                                                                                                                                                                                                                           WP1; ZUUÜ-452400/39.
                                                                                          (CHIR ) CHIRON CORP.
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Secure 58.4; DB 21; Length 1865;

17.18;

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Rest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                    AAA70476;
Query Match
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                                       Matches
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                                                                                                                                                                                 AAA70476
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                                                                                                         9
                                                                                                                                                                                                                                  The present sequence is the coding sequence of a HTV Gag protease expression cassette, Gagreot.ModS. The Gag protein of HTV is needed for the assembly of vitas like particles, in addition, the day protein is have load in ment states of the HTV lite cycle, including assembly, vitron maturation after particle release and early post entry steps in viral replication. The expression research may then be used for the recombinant expression of HTV Gag Folypeptides which may then be used to vaccinate against HTV intection and acquired immunodeliciency syndrome (AIDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV dag professe expression cassette coding sequence GagProtMod.SF2(GP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant expression of HIV dag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome
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                                                                                                                                                                                                                                                                                                                                                              862. gaeaticogecagggedenaaggageeettingergaetacgaeeeettingaeegettintaeaagaee 1921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barnett S, Zer Meqede J, Srivastava I, Lian Y, Hartog K, Liu H;
Greer C, Seiby M, Walker C;
                                                                                                                                                                                                                                                   97, 4%; Score 58,4; bit 21; Length 1853; 98, 4%; Pred, No. 2,8e-09; inc. 2, Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV I; AIDS; Gay profease, varrine, expression cassette; ss.
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                                                                                                                                                                                              Sequence 1853 BP; 421 A; 624 C; 580 C; 228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeticiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA70475 standard; DNA; 1865 BP
 Claim 5; Fig 7; (Olpp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               980S-5114495.
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                                                                                                                                                                                                                                                                    Best Local Similarity 98.99
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHIR.) CHIRON CORP.
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                                                                                                                                                                                                                                                       Duery Materia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression cassette, GaqProtMod.SF2(GP2). The Gaq protein of HTV is needed for the assembly of virus-like particles. In addition, the Gaq protein is involved in many stages of the HTV life cycle, including
                                                                                                                                      Gaps
                                                                                                      ), ganatividin addgenininaadgagninittiin ar dan tan gtadan (anttrittaaqan) (60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 gaeat.cogcougggeenenaggageest.teegegachaegtggaeegettetteaagaee 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the coding sequence of a HTV Gag proteuse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barnett S. Sur Megede J. Srivastava I. Lian Y. Hartog K.
Greer C. Selby M. Walker C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-1; AIDS; Gag-protease; vaccine, expression cassette: ss.
                                Indels
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0; Mismatches 1
Pred. No. 2.8e-09;
                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeticiency virus type 1.
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   78. 38;
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                                59; Conservative
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WPI; 2000-452400/39.
                                                                         (CHIR ) CHIRON CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200039302-A2.
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                   30-DEC-1999;
                                         31-DEC-1998;
                                                   01-PEC-1449;
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06-JUL-2000
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                                                                                               Barnett S,
                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                         Greer C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA70472
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                                                                                                                                                                                                                                                                                                                                               The present sequence is a HIV Gag/Hepatitis C virus (HCV) core fusion coding sequence. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post entry steps in viral replication. The present invention relates to synthetic HIV Gag expression cassettes. The present sequence was cloned and used to generate the expression cassettes of the present invention. The expression cassettes may be used for the recombinant expression of HIV Gag-Polypeptides which may then be used to veccinate against HIV infection and acquired immunodeficiency syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV Gag-polymerase expression cassette coding sequence GagPol.ModSF.
                                                                                                                                                                                                                              2ur Megede J, Srivastava I, Lian Y, Hartog K, Liu H,
tby M, Walker C;
                                                                                                                                                                                                                                                                                     Expression cassettes encoding the human immanodeficiency virus (HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58.4, UB 21; Length 2031;
Pred No. 2.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-1; AIDS; Gag-polymerase; vaccine; expression cassette; ss
                                                                                                                                                                                                                                                                                              Gag-containing polypeptide useful for vaccinating against HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                         infections and acquired immunodeficiency syndrome (AIDS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2031 BP; 421 A; 707 C; 646 C; 257 T; 0 other;
                                                      HIV-1; AIDS; Gay; vaccine; expression cassette, ss.
                                 Synthetic HIV Gag/HCV core fusion coding sequence.
                                                                          Chimeric - Human immunodeficiency virus type 1. Chimeric - Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                               Example 1; Pages 341·342; 391pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1.
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98.38;
                                                                                                                                                                                      99US-0168471.
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                                                                                                                                                                           98US-0114495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98 3%
             28-NOV-2000 (first entry)
                                                                                                                                                                                                            (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                 WP1; 2000-452400/39.
                                                                                                                                                                                                                                           Selby M,
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                                                                                                                                                        30-DEC-1999;
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                                                                                                                                                                                                                                 Barnett S,
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The present sequence is the coding sequence of a HIV Gaq-polymerase expression cassetts, Gaqpol Woose The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post entry steps in viral replication. The expression cassette may be used for the recombinant expression cassetted may then be used to vaccinate agains! HIV intertion and acquired immunodeficiency syndrome (AIDS).
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                                                                                                                                                                                                                                                                                                                                                                                 Expression cassettes encoding the human immunodoficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.3%; Score 58.4; DB 21; Length 4319; 98.3%; Pred. No. 3e-09; 1, Todels 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                   , Zur Megede J, Srivastava I, Lian Y, Hartog K, Selby M, Walker C;
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C;
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ilby M, Walker
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Matches 59; Conservative
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                                                                                                                                                                            The present involving relates to equitation HIV Gag and Environgers: observed in the day protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV like eyele, including assembly, virion maturation after particle release and early post entry steps in Viral replication. The expression cassettes may be used for the recombinant expression of HIV
                                                                                                                                                                                                                                                                                                                                                                                                                Gags and Envipolypeptides which may then be used to vaccinate against HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             control of a single CMV promoter and between the two coding sequences an internal Ribosome Entry Site (RRS) is present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                intection and acquired immunodeliciency syndrome (AlbS). The present sequence is a synthetic construct constructed in the generation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bicistronic in that the coding sequences for Env and Gag are under the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.3%; Score 58.4; bis 21; Longth 4472; 98.3%; Pred. No. 3e-09; ive 0; Mismatches 1; Indels 0;
Gay containing polypeptide useful for vaccinating against HIV
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                                       intections and acquired immunodeticiency syndrone (AIDS)
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Selby M. Walker C:
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                                                                                                          Claim 21; Fig 64; 491pp; English
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particle release and early post-entry steps is viral replication. The expression cassettes may be used for the recombinant expression of HIV Cag and Ery polypeptides which may then be used to vaccinate against HIV
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efrective of particles in addition, the Can protein to involved in many
stages of the HIV lite eyele, including assembly, virion maturation after
                       dag- and Env-polypeptides which may then be used to vaccinate against HIV
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                                                                                                          bleistranic in that the reding sequences for Env and Sag are under the control of a single CMV promoter and between the two coding sequences an
                                       infection and acquired immunodeliciency syndrome (AIDS). The present sequence is a synthetic construct constructed in the generation of the expression cassities of the present invention. This construct is bleisticate in that the redding sequences for English and are under the
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cassed for any becaused for the recombinant expression of HIV
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                                                                                                                                                                                                                                                               97.3%; Score 58.4; DB 21; Length 4608; 98.3%; Pred. No. 3e-09;
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                                                                                                                                                                                                                                                                                                         1; indels
                                                                                                                                                                                             Sequence 4608 RP; 1001 A; 1580 C; 1382 G; 645 T; 0 other;
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                                                                                                                                                     Internal Ribosome Entry Site (IRES) is present.
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Query Match 97.3%; Score 58.4; DB 21; Length 4689; Best Local Similarity 98.3%; Pred. No. 3e-09; Matches 59; Conservative 0; Mismatches 1; Indels 0; Saps
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Search completed: August 8, 2001, 18:25:01 Job time: 12605 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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SUMMARIES

Description	AF201927 Synthetic	AF202464 Synthetic	AP202465 Synthetic	AF287354 Synthetic	AF287352 Synthetic	AF287 353 Synthetic	AX019132 Sequence	AX035454 Sequence
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VEEKÄPSPEVIPMESALSEGATPQDLNTMLNTVGGHQAMQMLKETINBEAAEWDRVH
VVHAGTTATOQMEEPPSOINGTTETLZPGATAWINNPPIPVETIVERNTIVGENTIVET
PMXSPTSIIOTPQGREPPEPVYDFPYKTIBAEQASQOVKNMMTETLLVONARPDCKT
ILKALGPAATLEEBMITACQGVGGPGHKARVLAEAMSOVTNPATIMMORGNERNQKKTV
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KIEEEGNKSKKKRÁĽQAAAAGIGNSKÚVSQNYPIVONLÓGWYHQAISPRTLNAWYKV
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LQSRPERTAPPEESPRIGEEKTTPSQKQEPTDKHLYPLITSLRSLFGNDPSSQ"
620 c 579 g 228 t
                                       AVNPGILLETSEGCROTTGOLOFSLOTGSEELKSLYNTVATLYCVHORIDVKDTKEALE
KIEFEONKSKKKAQQAAAAAGTGNSSQVSQNYFLVUNLOGGWVHGAISPRTINAWVKV
VERKAESFEVTPPREALSECATPODLATMINNYGHQAAMWKKET NERBARWRWH
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PMYSTPSTLDIPOGPREPPROYDRPYKTLARAGASQUVKNAMTETTLVONARPDFYT
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                              /translation="MGARASVLSGGELDKWEKIPLPPGGKKKYKLKHIVWASPELFRF
                                                                                                                                                                                                                                                                                                                                                                                                     zur Megede,J., Cher,M.C., Doe,B., Schaefer,M., Greer,C.E.,
Selby,M., otten,G.R. and Barnett,S.W.
Increased expression and immunogenicity of sequence-modified human immunodeficiency virus type 1 gag gene
J.Virol. 74 (6), 2628-2635 (2000)
                                                                                                                                                                                                                                                                                                AF202464 1847 bp PNA SYN 12-MAP-2000 Synthetic construct gag-protease fusion protein GP1 gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-NOV-1999) Vaccines, Chiron Colporation, 4560 Horton Street, Emeryville, CA 94608, USA Location/Qualifiers
                                                                                                                    LOSRPEPTARPERSPREBETTPSOKOEPIDKELYPLISLKSLEGNDESSQ"
543 c 479 g 159 t
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                                                                                                                                                                          97 3%; Score 58.4; DB 56; Length 1509; 98.3%; Pred. No. 6.2e-07; tive 0; Mismatches 1; Indels 0;
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/protein_id="AAF42819.1"
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/product-"qag protein"
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/db_xref="G1:7248703"
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zur Megede, J. and Barnett, S.W.
Direct Submission
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L220A6 Human immun
AP2A6235 HTV-1 str
AF319334 HTV-1 iso
AF319356 HTV-1 iso
AF319356 HTV-1 iso
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U73073 HIV 1 1551a
AF100450 HIV 1 1550
AF106451 HIV 1 1550
AF106451 HIV 1 1550
AF106451 HIV 1 1550
                                                                   AF110975 HIV-1 iso
AF110973 HIV-1 iso
AJ24196 Human imm
AJ274561 Human imm
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Selby,M., Otten,G.R. and Barnett,S.W.
Increased expression and immunogenicity of sequence-modified human
immunodeficiency virus 1 year gene
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AF286234 HIV-1 str
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AF110974 H1V-1 iso
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/db_xref="taxon:32630"
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zur Megede, I. and Barnett, S.W.
Direct Submission
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/transl_table=11
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KCENTOKEGHTARNGEAPERKOGHRODERGHAMFDYTEPQANFLGKTINPSYKGEPGNF
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/db.xret="G1:7229427"
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Increased expression and immunoquicity of sequence-modified human
immunodelleitency virus type 1 deg gene.
J. Virol. 74 (6), 2628-2635 (2000)
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/product."qaq-protease fusion protein GP2"
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98.3%; Pred. No. 5,90-07;
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AVPPSLETTSPPSPBFFF SELEPPS SPPSPPFBBFFFN VATAPVHEK FENERE KEELE
KTEEEQNKSKKKAQQAAADTGNSSQVSQNYPTVONLJOOJMVHQATSPRTLINAWVKVVE
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YSPTSTLFFLPQDPFEPFPVVPPFYFTTRAFQASGEVRNWMFETLLVQNANNPPSKTTL
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                                                                                                                                                                                               Submitted (12-JUL-2000) Chemical Pathology, Women's and Children's Hospital, 72 King William Road, North Adelaide, SA 5006, Australia Location/qualifiers
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Submitted (12 JUL-2006) Chemical Pathology, Women's and Children's
Hospital, 72 King William Road, North Adelaide, SA 5006, Australia
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                                                                   Helper plasmids for production of HIV derived we tors Unpublished
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/product "qaq protein"
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1 (bases 1 to 4452)
Fuller,M. and Anson,D.S.
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Fuller, M. and Anson, D.S.
                                                                                                                         2 (bases 1 to 1548)
Fuller, M. and Anson, D.S.
                     1 (bases 1 to 1548)
Fuller,M. and Anson,D.S.
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RTRGAHTNDVKQLTBAVQKTAFESTVTMGKTPKFKLPTQKETMETWITESIYQATMTPE
WEFVNTPPLVKLWYQLEKEPTTGAETFYVDGAANRETKLGKAGYVTNKGRQKVVSLTÛ
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DITATDIGTKELOGAITKLOKFPYYPKISH-PI-WKGFAFKIJWKGEGAVVIQDNSDIKV
VPKKKAKIIRDYGKÇMAGDDCVAĞKQUED"
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KVYLAWVPAHKGIGGNEQVDKIVSAGIRKVLETDGITDKAQEEHEKYHSNWRAMASDEN
                                                                                                                   /translation="mgarasylsageldkwekirlrepggkkgyrlkH1Vwasrelfrf
AVDPGLLETSEGCRQ1LGGLQPSLQTGSEELRSLYNTVATLYCVHQK1EVKDTKBALE
                                                                                                                                                                                        EKAPSPEVIPMESALSEGATPQDLNIMI,NTVGGHQAAAQMLKETINEEAAEWDRLHPV
HAGPIAPGGMREPRGSDTAGTTSTL,GEGTGWMTNNPPIPVGETYKRWIII,GLNKIVRM
                                                                                                                                                                                                                                                             KALGPAATLEEMMPACGGVGGGGKARVLAEAMSOVTNSATIMMORGNFUNGKKTVKG
PNGGKEGHLAKNCRAPEKKGGWRGGKEGHQMKD:"TERGANFLGKTWPSHKGRPGNELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tränslation-"REDIAFPQGKARKFSSEQTPANSPIPFEPGVWFFINNSI.SFAGA
DRQGTVSFSFPQITLWQRPI.VTIKIGGGI.KFALLIDTGADDTVLEEMNLPGRWKPKMIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPVKLKPGMEGPRVKQWPLTERTIKALVETCTEMEKBSKTSKTGPFNPYNTPVFATKK
KDSTKWPKLVDFPFLNKFTQDFWEVQLGTPHPAGLKKKKSVTVLDVGDAYESVPLHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QYMDULY VGSDLETGQHRTK TEELRUHLLKWGF 11 FDKKHQKEPPFIJMIGY ELHPDKW
TVQP IVI,PEKDSWTVND I QKLVGKLINMASQIYAG I KVRQI I XKLLKGTKALTEV I PILTE
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                                                                                                                                                                                                                                         YSPTSILDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNWMTETLLVQNANPDCKTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIGGF LKVKQYDQIPIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFPISPIET
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                                                                                                                                                                KIEEEQNKSKKKAQQAAADTGNSSQVSQNYPIVQNLQGQMVHQAISPRTLNAWVKVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic construct HIV-1-derived gagrool fusion protein gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U; Gaps
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                                                                                                                                                                                                                                                                                                         SRPEPTAPSEESVRFGBETTTPSQKQEPIDKELYPLASLRSLFGSDPSSO"
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Prod No 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helper plasmids for production of HIV derived vectors Unpublished
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                                                                                                                                                                                                                                                                                                                                                             /note-"codon optimized reading frame"
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                                                                                                                                                                                                                                                                                                                                                                                                                           /product="pol_protein"
/protein_id="AAG28735 l"
/db_xref="G1:11066863"
                                                 /product="qay_protein"
/protein_id="AAG28735.1"
/db_xref="GI:11066862"
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Fuller,M and Anson,D.S.
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                                                                                                                                                                                                                                                                                                                                                                                      /codon start-1
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88.3%;
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synthetic construct
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Matches 53; Conservative
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HAGPIAPGOMREPROSDIAGTTSTLOROIGWMTNNPPIPVGEIYKRWIILGLNKIVRM
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FNCGKEGHTAKNCPAPFKKGPMKN3FEGHUMKTATLERGANFLREDLAFPGGKARKFSS
EQTRANSPTREERGVWRRDNNSLSFAGADRQGTVSFSFFYJTLMGRPFYTTKTGGGLK
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PTPVNIIGRNILTQIGCTLNPPISPIETVPVKLKPGMDGPKVKQWPLIEKKIKALVET
CTEMEKEGKISKIGKPENPYNTPVFAIKKKDSFKWKKLVDFRELNKRTQDFWEVQLGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGSPAIFQSSMTTILEPFRKQNPDLV1YQYMDD1.YVGSDLEIGQHRTKIEELRQHLI.R
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ELOKOGOGOWTYOIY VEPPKNLKTGKYAPTFGAHTNDVKOLTBAVOK IATESIYIWGK
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TAVQMAVFIHNFKRKGGIGGYSAGERIVDIIATDIQIKELQKQIIKIQNFRVYYRDSR
                                                                                                                                                                                                                                                                                                                                     *Lablation "MCAPASVESARELR*WEPTPEPGGFFQFPLFHTVWASRELERF
                                                                                                                                                                                                                                                                                                                                                                     AVDPGELETSEGGPQ11.AQLQPSLQTGSEELRSLYNTVATLYCVHQK1EVKDTKEALE
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                                                       /note="derived from Human immunodeficiency virus type 1
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MITPOPHANOHS KYPIACOS (GB); KINGSMAN ALAN JOHN (GB); OXFORD
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                                                                                                                                                     /note="codon optimized reading frame"
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                                                                                                                                                                                                                                                /product="gag-pol fusion protein"
/protein_id="AAG28737.1"
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88.3%; Pred. No 0.00023;
Five 0; Mismatches 7;
/organism="synthetic construct"
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AX019132
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                                /db_xref="taxon:32630"
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                                                                                           isolate YU-2"
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1 (bases 1 to 4307)
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UDEN MARK (GB) : OXFORD BIOMEDICA LTD (GB) ; MITROPHANOUS KYRIACOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Znote "gagpol-SYNqp- codom optimised gagpol sequence"
                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                        1 ducate sporandore or anguados ditesorques tangingas equits disagnas 39
Score 47.8; DB 9; Length 4307;
Pred. No. 0.00045;
0; Mismatches 7: Indels 0;
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Best Local Similarity R8 1%; Fred No 0.00045;
Matches 52; Conservative 0; Mismatches 7; Indels 0.
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Zdb 8ret-"taxon 325.82"
Zdoto "Godon optimised gagpol sequence"
i 1198 c. 1285 q. 689 t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              artificial sequence.

[ (dases 1 to 4407)
Mittephanous, K., Kim, N.H. and Kotsopoulou, E.
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/organism·"synthetic construct"
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AXD35453
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AX056836
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   79.78;
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Matches 52; Conserv
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Anti-viral vectors
Patent: Wo 0055341-A 14 21-SEP-2000;
UBEN MARK (GB) ; OXFORD ELOMEDICA LID (GB) ; MITROPIANOUS KYRIACOS
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/hote:"psyNGP3 - codon optimised BIV-1 gaqpol with leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actorism "synthetic construct"

/db.xrcf "taxon $26.80"

/note "psynGP4 - codon optimised HIV-1 qaqpol with 20 bp

/ note "psynGP4 - codon optimised HIV-1 qaqpol with 20 bp

/ note "psynGP4 - codon optimised HIV-1 qaqpol with 20 bp

/ note "psynGP4 - 69.84 to 1296 q 69.84 to 1296 p
1 gacatecqueaqqqevicaaqqaqevitticqeqaactarqtqqariqettitticaaqar 59
| HTHTHIII | HTHT HTHT HTHTHIHHHHHHHHHH HH HT H
| 870 GACATCCUCCAAGGCCGAAAGGAACCTTTCGCGACTAGGACGGGTTCTACAAAAC 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.7%; Score 47.8; D8.9; Langth 43.27;
88.1%; Pred. No. 0.00045;
Live 0; Mismatches 7; Indels 0;
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88.1%; Pred. No. 0.00045;
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Patent: WO 0055341-A 13 21-SEP-2000;
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AX035464
                                                                                                                                                                   Sequence 14 from Patent W00055341.
AX035465
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1. .4327
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1 (bases 1 to 4353)
Uden, M. and Mitrophanous, K.
                                                                                                                                                                                                                                                                                                                                                                   Uden, M. and Mitrophanous, K.
                                                                                                                                                                                                                            AX035465.1 GI:11191107
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1 (bases 1 to 4327)
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Hest Local Similarity 88.1%
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AUTHORS JOURNAL

FEATURES

REFERENCE

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Johnson, C. (bases 1 to 9010)
Novitsky,V.A., Montano,M.A., McLane,M.F., Renjifo,B., Vannberg,F.,
Novitsky,V.A., Montano,M.A., Marlink,R. and Essex,M.
Direct Submission
Submitted (03-DEC 1998) Immunology and Infectious Diseases, Harvard Submitted (03-DEC 1998) Immunology and Infectious Diseases, Harvard School of Public Health, FXB-310, 651 Huntington Avenue, Roston, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Lianslation "MCARASRLEGHKLD1WEKIRLEFGGEKGYMLFHIVWASPELFPF
                                                                                                                                                          /translation="PluquidgoQMVHQAISPRILNAWVKVVEEKAFSPEVIPMFSALS
EGATFODLNTMINTVGGHQAAMQMLKETINEEAAEWDRLHPVHAGPIAPGOMREPRGS
DIAGTISTLGEGIGWMTNNPFIFVGEIYKRWIIGINKIVRWYSPTSTINTRGGPKEP
PRDYVDRFYKTIRAEQASQEVKNWMIETLLVQNANPDCKTILKALGPAATLEEWMTAC
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I (basca 1 to 9010)
Novitsky V.A., Montano, M.A., McLane, M.F., Renjifo, B., Vannberg, F.,
Foley, B.T., Ndung'u, T.P., Rahman, M., Makhema, M.J., Marlink, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular cloning and phylogenetic analysis of human
immunodeficiency virus type 1 sublype C: a set of 23 full-length
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKG 02-MAR-200
HIV-1 isolate C-96BW15CU2 COUNTY BOUSWana, complete genome.
AF110974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human inmunodeficiency virus type 1.
Human immunodeficiency virus type 1
Viruses, Retroid viruses, Retroviridae, Lentivirus, Primate
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                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                         63.7%, Score 38.2; DB 58; Length 693; 78.0%; Prod. No. 0.37; 21ve 0; Mismatches 13; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product."gag.pol polyprotein"
/protein_id="AAD17126.1"
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J. Vitol. 73 (5), 4427-4432 (1999)
99214383
                                                                                                                      /protein_id="BAA93787.1"
/db_xref="GI:7416277"
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/country="Botswana"
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                                                                                                    /product="qag protein"
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                                      /qene-"qaq"
/note~"p24 region"
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/gene="pol"
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/dene-"dag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamada, T. and Iwamoto, A. Comparison of proviral accessory genes between long term nonprogressors and progressors of human immunodeficiency virus type
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                                                                                                                                                                                                                                                                                                                   Anti-viral vectors
Patent, Wo 6055341-A 12 21-SEP-2000;
UDEN MARK (GR) ; OXFORD BIOMEDICA LTD (GB) ; MITROPHANOUS KYRIACOS
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/note="psynop: - codom optimised HIV-1 dagpol with leader
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Pred. No. 0.00044;
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1. .693
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                                                                                             Sequence 12 from Patent WO0055341. AX035463
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/db_xref="taxon:11676"
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88.18;
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Hest Local Similarity 88.1%
Matches 52; Conservative
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AB034323

RESULT

KEYWORDS

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FEATURES

/db_xrol="G1:4:124865" /translation="MEPVPPKIEPWNHP3SyPKTPCTKGFCKGGSYHCLVGFUTKGLG ÖWTYG IYGEPERNI KTORYAKMETAHI NIVRGI GLAAVOR IAMENLYIMGKTPREPLI OKETWETWWTDYWGATWI PEWEYNI PPLVE, WYGGER PPLIGAELFYVEGAANESI K ALNPGLLET SPGCKO IMKOLOPALOTOT PELESTENTVAT LYCYHEK IKVKETESALD KTEEPUNKSGEKTOJAFAAAAKTSGAVPTVUNTGAMAHOATSPETTNAWVKVTPERA FSPEVTPMFTALSEGATPOJATNIATVGGHOAALOMIKDTTNEEAAEWDKLBDVHAG PIAPGOMREPEGSDIAGTTSTLOEGIAWMTSNPPLPVGDIYKKWIILGINKIVRMYSP VSTLDTRØGPREPFRDYVDRFFRTLRAEGATGDVRNWMTDTLLVQNANPDCRTTLRAL OPGATLEEMMT ACQGVGGPGHKARVI.AEAMSGATSANTLMGRSNPKGPKRTTKGF NCG DOTVI.EEMSI.PGKWKPKMTGG1GGP1KVRQYDQ1L.EETGGKKAIGTVL1GPTPVN11G KSVTVLDVGDAYESVPLDEDERKYTAFTTPSTNNFTPGTRYQYNVLPQGWKGSPSTFQ KHOKEPPELWMGYELHPDKWTVQPTELPEKESWTVNDJQKLVGKLNWASQ1YPGTKVR OLCKLI PGTKALTDIVPLTEEAALLIAENREITLREPVHGVYYDPSKDLVAEIOKOGHD PORSESELVNGT FROTTFRERVELSAVPAHEG GONEG GALVSAGLERVLE LOGGIDE AQEEHEKYHSNWRAMASFENLIPTVARETVASCIRCQLKGEATHGGVDGSPGTWGLDG AAVKAATWWAGTODEEG IPPNINGSGOVESMIN ELIKKTI GOVPDOABEHLKTAVQMAVE THNEKERGGI GGYSAGELTIDI TATDI QITKEL ORQITELI ONERVYYEDSRIPIWKGPA ALNIPOLLETSEGCKQ1MKQLQPALQTGTGELKSLENTVATLECVHEK1KVKDTKEALD K LEEEQNKSOEKTOOAEAAAGK LSONY P LVONLOGOMYBOA LSPRTLNAWVKV LFEKA ESPEVTPMETALSEGGATE_QDIATMINTVOGGGAAAL_QMILADT INEEAAEWDELHEVHAG PTAPQQMREPRGSDIAGTTSTI_GEGTAWIYSNDPTPVGDIYKPWITIGT NKTVPMYSP VSTIJDTRGGPREPERDYVOPEFRYIJAAPQATGOVRNWITDTIJVQNANEPDZRTTIJRAI. GROATIJEBMITAOQOVODSOHRABVIJAFAMSQATSANTIJNGBSNEROFREFTROFRYS At rains La Lion - "Menewgali vwovidemki ktwinsluvkhimy vskrtingwe yrihe Besphirk vskryti ptogram i vittywa ngystebeshi obsvstemklery strovingli. Aboli i Hmyyfologram i prami och i vitekovygagenk vossi oylalitali i projet Pplipsvrki vetopmik pokthorpomennii". OF 13H IMORGAPH WPOAPPLOOF PARMAL FOR FOR A CONTRACT OF STATE OF STATES OF S ISYARKKEGRRSAPPRSEDHONLISKOPLPRTGGDSTGSPESKKKVESKTETRRFF" KEGHTARNGRAPRKKGGWRGGREGHOMKINTI BIKQANFFREDIJAFPUGRAPFFPSFQNP ANSPTSRELÖVRÖDNPRSEAGAEROCTT.NFPQTTLMQRPLVSTRVGGGTREALLDTGA RNMLTQLGCTLNFPISPIETVPVKLKPGMM3PKVKQWPLTEEKIKALTAIGEEMEKEG KITKIGPENPYNTPVEAIKKKISTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKK SSMTK (LEPFEARNPETVIYGYM) og YVCSIG PICQHPAR I PELPFRI LPMGE 1950E IGKAGYVTERSREKTVSI TETTNEKTET EATEI ALEISSSEVNI VTESEVALSTI GELEA THEBORT HOVAVHVASGY LEAEV LPAETGQPTAYY HALAGBWPYRV FHTPNGSMPTS ZELODS LOT LOG - "MCARASRI KOFKLINIMEK LRIEPOSKKO'YMI KBLVWASPELERE KEGHTARNGRAFFRRGGWFGGREGHÇMKI» (FPGANFLOFTWPSBFOPPGNFLÇNPTF YTYETYGDTWTGVEALIRILOOLLFTHFRIGGLHSRIGIMRQRRARNGASRS" NILIWKGEGAVV IQUNSDI KVVPRKKVET I RIYGKQMAGAUGVAGRQUER!" PTAPPAESFKEFETTBAPKQFPKDFPLTSUKSLFGSOPTSQ* join (5297, 15521,7836, 17926) Agene "Lat" /product-"qaq polyprotein" /protein_id-"AAD17125.1" /db_xref:"Gi:432486i" /protein_id+"AAD17127.1" /db_xret+"G1:4324863" /protein_id-"AAD17128.1" /db_xret-"GI:4324864" /protein_id:"AAD17129.1" /codom start] /codon_start l /codon_start 1 /codon_start-1 /product-"Vit" /product - "Vpr" /product-"Tat" 5086 4508. .5086 /qene."vif" 9185 "Idv" =onop/ /qene "tat." " Inge" - remember /dener"rev 5026. 4508.

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                                                                                                  Translation "MAGPSFDSDFALLHAVPLIKTLYQSNDYPFDRGTPQAPKNKRR
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ORGANISM

KEYWORDS VERS ION

REFERENCE AUTHORS

TITLE

PEPEPENCE AUTHORS

MEDLINE PUBMED JOURNAL

JOURNAL

TITLE

FEATURES

ALNPGLLETSEGCKQIVKQLQPALQTGTEELPSLFNTVATI YOVHFY IKVKPTKEALD

gene

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QLÖKLLRGAKALTDIVPLTEBAĒLELAENKBILREPVHGVYYDPSKDLVARIQKOGHD
QWTYQIYQEPPKNLKTGKYAKMRTAHTNDVKQLTBAVQKIAMESIVIMGKTPKFRLPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGKAGYVTDRGROKIVSLTETTNOKTELQAIQLALODSGSEVNIVTDSQYALGI1QAQ
PDKSESELVNQIIEQLIKKEKVYLSWVPAHKGIGGNEQIDKLVSKGIKKVLFLDGIDK
AQEEHEKYHSNWRAMASEFNLPPIVAKEIVASCDKCQLKGGAIHGQVDCSPGIWQLDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THIBERTILIVAVHVASGYTEAEVIPAETGOETAYYILKIJAGRWPVKVIHTDNGSNFTG
AAVKAACWWAGTQOESGIPYNPGSGGVVESMNKELKKIIGGVRDOAEHLKTAVOMAVF
IHNFKRRGGIGGYSAGFRIIDIIATDIQSKELUKOITKIQNFKYYRDSRDPIWKGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MGAKASILRGEKLDAWEK!RLRPGGKKCYMLKHIVWASRELERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDTVLEEMSIPGKWKPKMIGGIGGFIKVROYDOTLIEICGKKAIGTVLIGPTPVNIIG
RNMLTQLGCTLNFPISPIETVPVKLKPGMDGPKVKQWPLTEEKIKALTAICEEMEKEG
KITKIGPENPYNTPVFAIKKRDSTKWFKLVDFPFINKPTQDFWEVQLGTPHPAGTKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /LFanslation="MGAKASILEGEKIPAWEFTPLPPGGKKCYMLKHIVWASPELERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLPQGWKGSPSIFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSMTKILEPFRARNPEIVIYQYMDDLYVGSDLEIGQHRAKIEELRKHLLRWGPTTPDR
KHQKEPPFLWMGYELHPDKWTVQPIELPEKESWTVNDIQKLVGKLNWASQIYFGIKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALNPGLI,ETSEGCKQ IVKQLQPALQTGTEELKSLFNTVATLYCVHEKTKVKDTKEALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPGATT.EEMITACOGYGGPGHKARVI.AFAMSOATSANILMORSNFKGPKRIIKCFNCG
KEGHTARNCRAPRKKGCWKCGKEGHQMKDCTERQANFFREDLAFPYGGKAREFPSEONR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKETWETWWTDYWQATWIPEWEFVNTPPLVKLWYQLEKEPIIGAETFYVDGAANRETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-DEC-1998) Immunology and Infectious Diseases, Harvard School of Public Health, FXB-310, 651 Huntington Avenue, Boston, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIEEEQNKSQEKTQQAEAAAGKISQNYPIVQNLQGQMVHQAISPRTLNAWVKVIEEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSPEVIPMFTALSEGATPQDLNTMLNTVGGHQAAMQMLKDTINEEAAEWDRLHPVHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIAPGOMREPRGSDIAGTTSTLOEQITWMTSNPPIPVGDLYKRWIILGLNKIVRMYSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANSPTSRELQVRGDNPRSEAGAERQGTLNFPQITLWQRPLVSIKVGGQIKEALLDTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novitsky,V A., Montáno,M A., Molane,M.F., Renjifo,B., Vannberq,F., Foley,B.T., Ndong'u,T.P., Marlink,R. and Essex.M.
Direct Submission
                                                                                                                                                                               lentivirus group.
1 (bases 1 to 9010)
Novitsky, VA., Montano, M.A., McLane, M.F., Renjifo, B., Vannberg, F.,
Folcy, B.T., Ndung'u, T.P., Pahman, M., Makhema, M. I, Marlink, R. and
                                                                                                                                                                                                                                                                                                                                        Molecular cloning and phylogenetic analysis of human
immunodeficiency virus type 1 subtype C: a set of 23 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVLWKGEGAVVIQDNSDIKVVPRRKVKIIRDYGKQMAGADCVAGKQDED"
                                                                                                                                   Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Human immunodeficiency virus type 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="gag-pol polyprofein"
/protein_id="AAD17135.1"
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/protein_id="AAD17134.1"
/db_xref="GI:4324870"
                                                              Human immunodeficiency virus type 1.
Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virol. 73 (5), 4427-4432 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:11676"
/country="Potswana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:4324871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"subtype: C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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AF110975 1 GI:4324731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dene-"pol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 9010)
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                                                                                                                                                                                                                                                                                                                                                                                                                        clones from Botswana
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                                                                                                                                                                                                                                                                                                                         Essex, M.
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STTLECASIAPATEAEVHWWAIHACVTICPRGEIELDIVTERHYMRUDWDDMHE
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RIRDKRQOYYALFYKLDIVPLNSNSSEYRLINCNTSALTQACPKVSFDPIPIHYCAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTANS LATION-"MVNFLAAKVDYRLGVGALIVALIIAIVVWSIVYIEYKKLLKOKK
IDWLIKPIPEPAEDSGNESPGDTEFLATWVDMGHLRLLDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /llauslation-"magksedsdeallhavriktlyqshryfefkgtrqakppppr
wrarqrqidsistrilstclgrpeepypfqlppteplnighsfsggtsgtggggggtte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /LIGHSIGLION="MEQAFEDGOPGREPYNEWALFILEELKOFAVRHFPPPWIHSIGO
YIYETYGDTRTGVKAIIRILQQLLFIHFRIGCLHSRIGIMRORPARHGASRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mepVDPKLEPWNHPGSHPKTPCTKCFCKGCSYHCLVRFOTKGLG
ISYGRKKRGGHRSAPPRSKOHQNLISKQPLPKTQGDSTGSBESKKKVESKTETDRFD"
                                                                   VSTIDTROGEKEPFELDYUDEFFKTI.KABOATQDVKMMTDTI.LVQNANPDCKTTI.RAL.
GPGATLEEMMTACQGVGGPGHKARVI.ABAMSQATSANTLMQKSNFKGPKRTI.KCFNUG
KESHTAENTFAPFKKGTWKOGKFGHQMKDCTFRQANFLGK.IWPSHKGBPSNFTQNRTE
                                                                                                                                                                                                                                                                                                                                                                                  ESKHPKVSSEVHIPLGEARLYIIIVWGLQIGERFWHLGHGVSIEWRLRRYSTOVDPGL
ADQLIHMYYPUCFAESAIKKAIFGHIVIPKCNYQAGHNKVGSLQYLALIALIKPKQIK
PPLPSVRKLVEDKWNKPQKIRGKRGNRTMNGH"
KIEEEUNKSÜEKTUÜÄEBÄÄGKISONYFIVONLOGOMVHUAISPRTINAMVEVIEEKA
FSPEVIEMETAISEGATPODLNIMLNTVGGHOAAMOMLKDIINERAABWDRLHDVHAG
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                                                                                                                                                                                                                                                                                                                                                                 /translation="MENRWQALIVWQVNRMRIRTWNSLVKHHMYVSKRTNGWFYRHHF
                                                                                                                                         PTAPPAESFKFEETTPAPKQEPKDREPLISLKSLFGSDPLSQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(5436 [55]],7836. βύβ3)
/gene="rev"
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/gene="tat"
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                                                                                                                                                                                                                                                                       /codon_start=1
/product="Vif"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"Vpr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"Rev
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5525.
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/qene="vpu"
                                                                                                                                                                               /gene-"vif"
4508. FART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5297. .7926
/gene="tat"
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/gene="env"
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/gene="vpr"
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63.7%; Score 38.2; DB 58; Length 9010; 78.0%; Pred. No. 0.18; Live 0; Mismatches 13; Indels 0; Gaps

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AF201927 Syntheric	AF287454 Synthetic	AF202464 Synthetic	AF202465 Synthertic	AF287.452 Synthetic	AF287353 Synthetic	AXU35453 Sequence	AX056836 Sequence
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Hospital, 72 King William Foad, North Adelaide, 8A 5006, Australia
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                                                                                                                                                                         zur Meqede,J., Chen,M.C., too.B., Schaeter,M., Orcer,C.E.,
Selby,M., Otten,G.R. and Barnett,S.W.
Increased expression and immunoquicity of sequence modified human
Synthetic construct gag-protease fusion protein GP2 gene, complete
                                                                                                                                                                                                                                                                                                                                                                                 Chiron Corporation, 4560 Horton
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95, Conservative 0; Mismatches 184; Indels 30; 0
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//product = 4aqq protease lusion protein GP2"
//protein_id="AAP4-AR20.1"
/db_xret="G1:7229427"
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/db_aret "taxon.32640"
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YSFTSTLDIPPPPPRYVDRPYYRTLAPEGOSOEVNAMPTETLIANDANDOKTTLL
YAKLGPAGTLEENWIRGCGVGGGGGHKARVLAPEAMSOVINSATIMMOKSNETNOKTIV
FUNGKEBHTANGTRAPPRKGGWKCGKFGHOMKDCTERQANFLGKINPSHKGRPGNFLO
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/db_xref="GI:11066862"
/translation "MGARASVLSAGELDFWER!PTPPGGFFGYPIKHIVWASPELERF
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Fuller, M. and Anson, D. S.
Fuller, M. and Anson, D. S.
Fuller, M. and Anson, D. S.
Fuller, M. and Anson, D. S.
Fuller, M. and Children's
S.Fuller, G. Full. 2000, Children's
Hospital, 72 King William Road, North Adelaide, SA 5000, Australia
Foration/Qualifiers
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/db_xref="taxon:32630"
/note="derived from Bounds immenodeficiency virus type 1 isolate YU-2"
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/product="pol protein"
/protein_id="AAG28736.1"
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/product="gaq protein"
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9; Mismatches 292; Endels 24;
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Direct Submission
Submitted (12 JHL 2000) Chemical Patholody, Women's and Children's
Bospital, 72 King William Road, North Adelaide, SA 5006, Australia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helper plasmids for production of HIV derived vectors \ensuremath{\mathsf{Unpublished}}
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1 (bases 1 to 4354)
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Fuller, M. and Anson, D.S.
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Anti-viral vectors
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1417 aaqqaccgcgagacretgaccageetqaaqageetgttegqeaacgacceetgageeag 1476
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                                                              1129 agcaacttoaagggcccccggcgrafegteaagtgcttoaactycygcaaggugggcccc 1188
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Viruses; Retroid Viruses; Retroviridae; Lentivirus; Primate
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Location/Qualifiers
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1 (bases 1 to 4307)
Mitrophanous, F. Kingsman, A. Land Kim, N. Anti-viral vectors
Patent: WC 9941397-A 2 19-AUG-1999;
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Sequence 2 from Patent W09941397.
AX019132
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UDEN MARK (GB) ; OXFORD BLOMEDICA LITO (GB) ; MITROPHANOUS KYRIACOS
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Actomism."synthetic construct"
Adb_xrel."tcsnn.32630"
Anote."psyMCP4 coden optimised HIV I qaapol with 20 bp
of the leader sequence of HIV-1, etc"
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Patent: WO 0055341-A 14 21-SEP-2000;
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Sequence 14 from Patent W00055341.
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/db_xret="taxou:32630"
/note="psyNGP3 - codon optimised HiV-1 gagpol with leader sequence from the major splice donor"
1198 c 1302 q 700 t.
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UDEN MARK (GB); OXFORD BIOMEDICA LID (GB); MITROPHANOUS KYRIACOS
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                                                                             sequence 13 from Patent WO0055341.
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1 (kases 1 to 433)
Uden,M. and Mitrophanous,K.
Anti-viral vectors
                                                                                                                         AX035464
AX035464.1 GI:11191106
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Novitsky,V.A., Montano,M.A., McLane,M.F., Renjifo,B., Vannberg,F.,
Foley,B.T., Ndung'u,T.P., Rahman,M., Makhema,M.J., Marlink,R. and
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Viruses, Retroid viruses: Retroviridae; Lentivirus, Primate
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GPLAPGQMKEPKGSDIAGTTSTLOEQIAWMTSNPPIFVGDIYKKWIILGINKIVKMYS
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LGFGASLEEMMTACGGVGGFSHKARVLABAMSGANTSVMMGRSNFKGPPRTVKFFNG
REGHTARNCRAPFRKGYWRGGREGHGMKLGCTERQANFTGKTNPSHKGRPGNFLGSRPE
PTAPPAESFREBETTPGUNGESKUKETLTSLRSLFGNDFLSG"
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PDKSESELVIQITEQLIKKERIYLSWVPAHKGIGGNEQVDKLVSSGIRKVLFLDGIDK
AQEEHFKYHCNWRAMASDFNLPPVVAKEIVASCDKCQLKGEAMHGQVDCSPGIWOLDC
THLEGKIILVAVHVASGYIEAEVIPAETGQETAYYILKLAGSWPVKVIHIDNGSNFTS
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THNIKRRGETGGYSAAHFI HTI TATDTGTKELOKQI IKTONFYYYPINSPIPVWKGPA
KLEWKGEGAVVIODNSDIKVVPRRKVKI IRBYGKONAGDBCVAGRODED"
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LEGRASLEDEMATACOGNOGESHKARVIVARAMSOANTSVMMOKSNEKGPRRIVKCFNUG
KESHIARNITAAFKRIVMKOGNEGHOMKOGTEDQANFFENIAFPURGESEGTTR
ANSFTSEELQVEGDNFFSETFVPROGNIPNFFOITLWOPPLINSIKVGGTFEBILDTGA
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KTEFERONKCOOKTOOAFAANKKVSUNYPIYONLOGOMVHGAISPRTLINAWKVIFEK
AFSPEVIPMETALSEGATPQDINTMINTVGGHQAAMOMLKDTINEEAAEWIPVHPVHA
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                                                                                                                            Submitted (03-DEC-1998) Immunology and Infectious Liseases, Harvard School of Public Health, FXB-310, 651 Huntington Avenue, Boston, MA
2 (bases 1 to 9007)
N. Witsky, V.A. Montano, M.A. McLane, M.F., Renjifo, B., Vannberg, F., Folgy, E.T., Ndung, J.F.F., Matlink, F. and Essex, M.
Direct Submission
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/protein_id="AAD17056.1"
/db_xref "G1.4324792"
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/protein_id="AAD17055.1"
/db_xref="G1:4324791"
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/db_xref="taxon:11676"
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/protein_id="AAD17061.1"
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NETWORDS SOURCE ORGANISM Human immunodeficiency vitus type 1 Viruses, Rettoid vituses, RettoVilidae: Lentivirus, Primate	
<pre>lentivirus group. teFFBRNCE i (bases 1 to 9006) AUTHORS NovitsKy.V.A. Montdano,M.A , M-Lan-,M F , Renjifo,B., Vannberg.F., Foloy,R T , Ndung'n.T P., Rahman.M., Makhema.M.J., Marlink.R. and</pre>	
ESSEX.M. TITLE Molecular cloning and phylogenetic analysis of human immunodeficiency virus type i subtype C: a set of 23 full tength clones from Botswana clones from Botswana H427-4432 (1999) MPDI.NE 99214383	
OURNAL SUBMITTED (03-DEC-1999) HMMUHOLOGY AND THECTLOUS DISCASES, MAIVALD School of Public Health, FXB-310, 651 Huntington Avenue, Boston, MA 02115, USA	

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Zdisymot="A1704-"m:STAATBYPTGWARVVALTTALTVWLTVYTEYPRT VPQRKTD
WLVRETPERARDSGNESIGDTFELSTWUMGHFPLLIDT"
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YTYETYGDTWTGVEALLKYLQQILETHFRIGCGHSKIGILRORKVRNGTNRS"
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WRAFORQTHSTSERTLSTCLGRPTEPVPFQLPPTERLHTDCSESSGASGTQRSGGTTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          school of Public Health, FXB-316, 651 Huntington Avenue, Buston, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novitsky,V.A., Montáne,M.A., Molane,M.F., Redjife,B., Vanderg.F., Foley,B.T., Ndung'u,T.P., Marlink,R. and Essex,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novitsky,V.A., Montáno,M.A., McLane,M.F., Fenjifo,B., Vannherg.F.
Foley,B.T., Ndung'u,T.P., Rahman,M., Makhema,M.J., Marlink,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunodeficiency virus type I subtype C: a set of 23 full-length
                                                                                                                                                                 ttegaggagecaceceeggecagaageaggaggageaaggacegegagacetgaceage 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1660 FILISAGISAGAGAAPPOPOSAFVASAAADAAGAGTOSAAGGAGAGAAAAATITAACTTCC 1719
                                                                      1021 etggaagagatgatgaeeqeetgeeagggegtgggeggeereeageeaaaggeeggegtg 1080
                                                                                                                                            1081 etggeegaggegatgageeaggeeaaceeaeegegtgatgatgatgaagaaagageaaetteaag 1140
                                                                                                                                                                                                                                                    1420 GGCCCTAGAAGAATTGTTAAATGTTTTAAAAGGGGAAAGGACACATAGCCAGAAAT 1479
                                                                                                                                                                                                                                                                                      tgeegegeeeeeegeaagaagggetgetggaagtgegaeaaggaggagggeeeeeegatgaag 1260
                                                                                                                                                                                                                                                                                                                                                            1261 gactysucsydyscupyscaacttectgggeaagaintggerenggennaagggeege 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKDD GYAGGGAATTTFCTTCAGAGCAGACCAGAGCAAGGGAGCGCGAGGAGGAGGAGATTTGAGA 1659
961 gippoagaabyocaabooogaatiybaaqaabattiitigogootootoogootoogaabaaqadaaga 1020
                                  02-MAR-2001
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Viruses; Retroid viruses; Retroviridae; Lentivirus, Primate
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J. Virol. 73 (5), 4427-4432 (1999)
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/count.ry="Botswana"
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ESRHPPVSSEVHIPLGDAPLVIKTYWGI (TGFPIWHLGHGVSIEWKLRKYSLOVDPGP
ADQLIHMHYFDGFADSAIRKALLGQIVSPRCEYQAGHNKVGSLQYLALTALIKPKKRK
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AġĠĠijĠĸŶijĊĸŴŖĄMĸŚŊŶŊŶŖŶŶĸĸŖŦVĄŚĊŊĸĊŖĹĸĠĠĸŢĦĠŷŶĎĊŚŖĠĬŴŎĹĎĊ
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LCPGASLEEMYTACQGYGGPSHKARVLAEAMSGTNTNVMMQRSNFKGPRRIVKCFNCG
KEGHIARNCRAPRKKGCWKGGKEGHQMKDCTERQANFLGKIWPSHKGPPGNFLGSRPF
PTAPPAESFRFEETTPVQKQEPKDRETLTSLKSLFGSDPLSQ"
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ALNPGLIETLEGCKOI LOGLOPALOTGEELKSLYNIVAILYCVHKKIEIKDIKEALD
KIEFPONKTOOKIOOAFANKKKVSONYPIVONIOGOMVHOAISPRTINAWKVIEEK
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KSVTVLDVƏDAYESVPLDESFPKYTAFTIPSINNSTPGIRYQYNVLPQGWKGSPAJFO
SSMTKILEPPRIKNPDIVIYQYMDDLYVGSDLEJGQHRAKIEELREHLLKWGLTTPDK
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KIEBEONKCOOKTOOAFAALKGKVSONYPI VONLOGOWYHOAISPRILNAWYKVIEEK
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THNPKRKGG1GGYSAGERTIDITATDIQTKELOKQIIKIQNFRVYYFDSRDPVWKGPA
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GPIAPCQMREPRGSDIACTTSTLQEQIAWMTSNPPIPVGDIYKFWIILGINKIVRMYS
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KEGHLARNCEAPPRKOOWKCGPFORGMKPCTEPGANFPPENTAFPORTAFPORTP
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PNMI TQLOCTINEPISPIETVPVKLKPGMDGPKVKQMPLTEEKIKALTAICEEMEKEG
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/protein_id="AAD17047.1"
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/protein_id="AAD17046.1"
/db_xref="GI:4324782"
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/db_xref="G1:4324785"
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/qene="vpr"
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/gene="vif"
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                                                                   280. .4562
/gene="pol"
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                                /qene="qag"
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280. .4562
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/protein_id="AAD17050.1"

/db_xx+d="01.4324786"

/translarion="MEPIDENI E-PRHHATS-DENIA"NETYPKHESYHETIVERGEGEG
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SGDKWIETLHWVSTKLAFHFPINKTTKFNSSSCODOLETTTRSFNÇEQFPFYÇNTSGFP
ESYWENETYGSNGTRATTTLPCRTKOTTNWWGYVGPAMYALPTAGNITGLLL
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LITVWG IKQLQTRVI AT FRYLKTGQLLG IWGYSGRT TOTTNV PWNNSWSNKST TV TWSN
MTWMEWDKETSNYSNT LYRLLEDSQNGOEKNEKDLLALGSWDST, RNWENYTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zprotein_id="Aadi17052.1"
Zdb_xret="01:4-8.4788"
Zdborslaffon="Mini Aavinvelgugaeivai italivwiivy eeyekivegeki
DWJVKE REBARDSORESJOSTEELSEMVDM/NALAGDDI"
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TSNIVAANNAACAMLEAGEEEEEVGEPVEPOVELEPMIYKAAVULSEELKEKGGLEGIT
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ENNKLLIPMSLAGMEDALXGEVLRWKFDSHLAYRHMARELIAPEYKDC"
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KATLFCASDAKAYDKEVHNVWATHACVPTDFNPQEVHLENVTENFNMMKNDMVEGMHE
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     Join (5296, 15510, 7863, 17953)
Agenje "fat"
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53.9%; Score 797.4; DB 58; Longth 9036; 21.2%; Prod. No. 16-81;

Best Local Similarity

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

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Mastigamoeba balamuthi. SM Mastigamoeba balamuthi Enkaryola; Mastigamoeba. E (bases lto 1674) S Lee,J.A., Moore, D.V., Gorden, P., Sensen, C.W., Gaasterland, T. Muller, W. Contrassed saminates from the free-living	Mastigamoeba balamuthi. SM Mastigamoeba balamuthi	X.						
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Leb.J.A., Moore, D.V., Corden, P., Sensen, C.W., Chasterland, T. Muller, M., Moore, D.V., Corden, P., Sensen, C.W., Chasterland, T. Muller, M., Cappers, M., Capp	l (bases 1 to 1674) Lec.J.A., Moore, D.V., Gorden, P., Sensen, C.W., Gaasterland, T. Moller, M. Muller, M. clones (expressed sequence tags) from the free-living amitochondists amoebollane. Masticamoeba halamithi		stigamoe. Garvota:	ba balan Mastiq	mathi moob	-		
Leo,J.A., Moore,D.V., Gorden,P., Sanson,P.W., Gaasterland,T. Muller,M. Child Clines (expressed sequence than the free-living	<pre>let.j.A., Monte,D.V., Gorden,P., Senson,F.W., Gasterland,T.Muller,A. cubA.clones (expressed sequence tags) from the free-living emitorhondists amoebollabellate. Masticamoeba halamithi</pre>		(bases	1 to 16	74)			
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.3%; Score 80.6; DB 148; Length 1674;
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0; Mismatches 756; Indels
                                                                                                                                                                     /organism="Mastigamoeba balamuthi"
Unpublished (2000)
Contact, maller miklos
Laboratory of Biochomical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmullersrockvax.rockefeller.edu
Insert Longth: 1674 Std Error: 0.00
                                                                                                                                     Location/Qualifiers
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Matches 615, Conservative
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HG314500 509 bp mRNA EST 16-APR-2001
WHE2495_E11_12122 Triticum monococoum early reproductive apex CDNA
library Triticum monococoum cDNA clone WHE2495_E11_121, mPNA
                                                                                                                                                                                                                                                                                                                                                                                                         :: lambda2AP; Site_1 FccRl; Site_2: Xhol"
184 g = 133 t = 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   604 alcaacgaggaggccgccgaglgggaccgcclgcacccqlgcaggccggccc---cglg 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             490 CGCTACTACCCCCGACTTCGTNCTCGACCTCAACAAGGCCCTCGCCGCCGACCAGCGCGTN 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 gacaagatcgaggaggaggagcagaacaagtcccagcagaagacccagcaggccaaggaggcc 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 CACAAGATCGACTTCGGCGAGGGCCGGGCTCCCGGTCCTGGACGCCCTCCTCGAGGAC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 caggecatcageeeneeqnannetgaaegeetgggtgaaggtgategaggaggaaggeette 483
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                                                                                                                                                                                                                                                                                                                /clone_lib="Wordsop Vilgare seedling root EST library
WvcDNA0007 (eticlated and unstressed)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 GAGATCACCACCAACCACCCATGSAACCTSAFCACGACGTCSGCGGAGAGAGGGCCAGTCC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 GAGGCCAACCACGCCACTTCGACTTCGTCTTCGTGGACGCCGACAAGGACAACTACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.1%, Score 76.4; DR 146; Length 759;
Rest Local Similarity 47.8%; Pred No. 0.00021;
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100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Seedling root"
/lab_host="TJC121"
                                                                                                                                                                                                                  /organism~"Hordeum vulgare"
                                                                                Email: rwing@clemson.edu
Sejprimer AATTAACGTTCAGTAAAAGG
                                                                                                                                                                                                                                                                                             /clone-"HVSMEf0019H19f"
                                                                                                                                    High quality sequence stop: 757.
                                                                                                                                                                                                                                        /cultivar="Morex"
/db_xref="taxon:4513"
                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 c
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                           Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Emblyophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Fooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wing, P. Close, T.J., Kleinhofs, A., Wise, R., Bequm, D., Frisch, D., Yu, Andersoc, H., Dale, J., Heary, D., Kernedle, S., Palmer, M., Pawke, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1307 giranaaaqqqooqooqqqqaaqtteetqeaqaaqrqqaqoqqqqqqqqqqqqqqqqqqq1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1390 GCGACATCTACCAGTCGCTCGACATCGCCTGGAGCCTCTGCG----CCAGTTCCCCAAGG 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1367 tannhanngnonnnennangagagetteeqetteqagagagageceeeceeeceee 1426
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1090 ACATCACCGAGGCCCAGATCTACGTCGACAGGAGCTGAAAAAAAGGGAGATCTACCGGC 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1330 CCCTGGAGTTCCTCCGAGAAGTFCGGAAGAAGTTCAFFACGFAGGGAGTAFAAAGAGTCGC 1389
                                                                                                                                                                                                                                                                         950 certgetggtgeagaacgecaaeceegaetgeaagaeeateetgegegeteteggeeeeg 1009
                                                                                                                                                                                                                                                                                                           1010 gegecaccetggaggagatgatgacegectgccagggegtgggeggeggergennggnnacaagg 1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1127 agagcaacttcaugggcccccggcgcaacgtcaagtycttcaartgryyraaggaggycr 1186
                                                                                                                                                                                                                  973 cGACCATCTACGAGCCTGCGGGCGTG---TCGAGGGCAGGAAGGGCTCGATCACGAGC 1029
                                                                                                                 890 tetteaagaeeetgegegeeggageaggeeaceaggaegtgaagaartggatgaeegaga 949
                                                            830 igageateetygaeateegeeageeagggeeeeaaggageeeiteegegaetaegtygaeeget 889
           853 ACGIGCIGGICALCCIGACGGACATGICGICGIACGCGAIGCCIACCICGCTGACHICLCGG 912
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Clemson University
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Unpublished (2000)
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//dev_stage__seven received to the seven plants of the stage of the stage of the seven prepared from apex at double-ridge stage to terminal-spikelet stage during transition from vegetative state to thower state, a club library was made.
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                                                                                                                                                                                                                                                                                                 Sperimatophyta: Magneliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Priticum.
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US Department of Agricallage, Agriculture Research Service, Pacific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JC.C., Kang,Y., Lazo,C.R., Willer,R., Raugch,C.J., Seaton,C. Stamova,B. and Tong,J.C.
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800 Bachanan Street, Albany, CA 94710, USA
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poulos, Ponocae, Ponoideae
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West Area, Western Regional Research Center
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//issae_lype-"Sgike belore anthesis"
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//dab_bost."E. coli SOLR"
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greenbouse. Whole spike with awns trimmed, white, green
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49 0%; Pred No 0 00063;
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rockefeller.0.10 Mastigamoeba balamuthi lambda 2AF II Library
Mastigamoeba balamuthi cDNA similar to tyrosine-phenol lyase, mRNA
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1230 York Avenue, New York, NY 10021, USA
Email: mmullerforckvax.rockefeller.edu
Insert Length: 1327 Std Error: 0.00
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Contact: Muller Miklos
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Iriticum aestivum
Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
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268 c 163 q 87 t
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Anderson, 0.0., Chao, S., Han, P.S., Hisia, C.C., Johnson, R.K., Kang, Y., Lazo, G.R., Miller, R., Fausch, C.J., Seaton, C.L., Tong, J.C., Verhey, S.D. and Walker-Simmons, M.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The structure and function of the expressed portion of the wheat genomes - ABA-treated embryo library
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Johnson (Colby College, ME/Walker-Simmons' lab). P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence have been trimmed to remove vector sequence and low-quality sequence with phred sovre less than 20 seq primer; Clondsoch Mitchfinker 3' AD primer.
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49.1%; Pred. No. 0.0028;
U.Se. 6 Mismateher, 248; Tobels 12.
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/dev_stage="Mature dormant seeds"
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- Web : www.genoscope.cns.tr)
- Web : www.genoscope.cns.tr)
- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Urosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information pricate see http://www.fruitly.org The HORD Prosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecokl digestion of Drosophila DNA provided by the BMCP from the isogenic strain v2: on bw sp. the same strain used for the BMCP's and an or the ST library of more detailed description of library or an extraction of Drosophila DNA provided by the BMCP from the strain v2: on bw sp. the same strain used for the BMCP is a fine of the library of the BMCP is an or the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of the BMCP of t
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Submitted (62-38N 1999) Genesesper - Centre National de Sequencaqe :
BF 191-91006 EVRY cedex - FKANCE (E Mail : sequelagenoscope.chs.fr
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/db_xret="taxon:7227"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Eurospan Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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1124 agaagagcaacttcaaggggcccccggcgcaacgtcaagtgcttcaactgcggcaaggagg 1183
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                                          Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
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/plasmid="pBeloBAC11"
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4.4%; Score 66.6; DB 219; Length 1101; 16.2%; Pred. No. 0.013;

Best Local Similarity 16.2%; Pred. No. 0.013; Matches 71; Conservative 197; Mismatches 171; Indels

Query Match

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/tissue_type="Leaf, crown"
/note="Vector: Bluescript Sk-/XhoI-EcoRI; Site_1: Eco RI;
Site_2: Xho I; Lower temperature 50 C / hour from 22 to
12.0C, bling to 50 in 1 hour from 120C. Leave at 50C 3 days
, photoperiod 16 hours. Light intensity was 125 uE-1.
Library prepared by in vivo mass excision from amplified
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Sigh,J.A., Wakuli,K., Couroux,P., De Moors,A., Harris,L.J., Hattori
,J.L., Ouellet,T., Robert,L.S., Sprott,D. and Tinker.N.A.
Expressed Sequence Tags from Cold-Stressed Maize Seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E0321263 813 bp mRNA FST 27-FFB-2001
Zmo4_04g04_P Zmó4_AAFC_F70PC_G016_Stressed_maize_seedlings Zea mays
CDNA clone Zm04_04g03, mKNA sequence.
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/clone_lib="Zm04_AAFC_ECORC_cold_stressed_maize_seedlings"
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Spermatophyta, Magnollophyta, Elliopsida, Poales; Poaceae; PACS
clade; Panicoldeae, Andropogomeae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agriculture and Agri-food Canada 960 Carling Aronno, RIA 006, Canada 160 Calling Aronno, RIA 20, Ottawa, Ontario, KIA 006, Canada Tel: (613) 759-1662 Fax: (613) 759-1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 tegaggaggageagaacaagteeeaqqeaqaagarrragraggeraaggaqqeegaeggea 370
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                                                       ESS OMSSOUGHSOSONSSIONSERARONVERAPOPOPAGGINASOACMAADOGGOARMACCSSS
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296 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                          34 % acrosayosayasayasayasayasayayayasayayasayaasayaasatacoccatrgtycagaac 402
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                                                                                                                                                                                                                                                                                                            463 gtgatogaggggettteageeetteageeetgaggggeeeatgtteaeegeeetgagegag 522
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1 (bases 1 to 585)
                                                      Ouery Match 4.4%; Score 56.2; DB 152; Longth 813, Best Local Similarity 43.2%; Pred. No. 0.015; Matches 809; Conservative 11: Mismatches 389; Indels 6;
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Full-length cDNA libraries and normalization
Unpublished (2001)
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Determination of this HAC end sequence was carried out as part of a collaboration with the Berkeley prosophila Genome Project (BBGP). The BBGP is constructing a physical map of the brosophila melanogaster genome using thirds. For further information please see http://www.fruitfly.org The BBGP lossophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                                                                                                                                                                                                /clone="CSODFOO3Y107"
//clone_lib="LTL_ETO15_FBrul"
//dev_stape="pooled rissue from post conception tetuses (20
week, 24 week and 26 week)"
                                                                                                                                                                                                                                                                                                                                            Anote-"Organ: Fetal brain; Vector: pCMVSPORT 6: 1st strand cDNA was primed with a Notl-oliquo(dT) primer. Five prime and enriched, double-stranded cDNA was diaested with Not 1 and cloned into the Not 1 and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Lite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Technologies. Centart: Ernq Hang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20950. USA Fax. (!) 60: 610 8371 Email: Hiangelitetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-JUN-1999) Genoscope Centre National de Sequencage BP 191-91006 EVRY cedex - FRANCE (E-mail : seqretagenoscope.cus.tr
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                     BP 191 91006 EVRY codex - France
Email: seqref@qenoscope.cns.fr, Web : www.qenoscope.cns.fr.
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Centre National de Sequencade
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    Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named MPCL'-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain of Drosophila DNA provided by the BDGP from the Isogenic strain wsc for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual RAC clones, the entire library or filters for hybridization from the BACPAC Personer Center can be
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1 (bases 1 to 901)
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web · www genoscope ons fr.
                                                                                                                                                                                  found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
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Matches 52; Conservative 172; Mismatches 138; Indels
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4.3%; Score 65.6; DR 106;
Bost Local Similarity 45.1%; Pred. No. 0.019;
Matches 274; Conservative 2; Mismatches 331; 1
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http://fulllength.invitrogen.com"
311 c 362 q 28 t
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/organism="Homo_sapiens"
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Mastigamoeba balamuthi eDNA similar to pyrophosphate--fructose
6-phosphate liphosphotransferase, mRNA sequence.
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43.4%; Pred. No. 0.021;
ive 0; Mismatches 521; Indels 9;
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1240 York Avenue, New York, NY 10021, HSA
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1 (bases 1 to 1427)
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Matches 407; Conservative
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Tel: 864 656 7288
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US Department of Agriculture, Agriculture Research Service, Pacific
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Boo Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeue; Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson, O.D. Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kara, Y., Lazo, G.R., Miller, R., Pausch, C.I., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF483204 419 bp mRNA EST 06.DEC-2000 WHE1787_B03_C05ZS Wheat pre-anthesis spike cDNA library litticum aestivum cDNA clone WHE1787_B03_C05, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
                                                                                                                                                                                                                                                                                                                                                                                               734 octggatgaccagcaaccccccgtgcccgtgggcgacatctacaagcggtggatcatcc 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614 aggeegeegaatgggaeegeetgeaceeegtgeaggeeggeeeeqtggeeeeggeeaga 673
                                                                                                    494 tgatececatgttcaeegeeetgagegagggegeeaeeeeeaggaeetgaaeaegatgt 553
                                                                                                                                             83 TGGRACCGCCTCGRACATGGRACTTTCGTGRACGGGCGCTTTCGACCACGCGGGAGT 142
                                                                                                                                                                                                   554 tgaacaccgtgggggggccaccaggccgccatgcagatgctgaaggacaccatcaacgagg 613
                                                                                                                                                                                                                                               06-286-2000
                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="WHE1787_B03_C05"
/clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
4 3%; Score 64.8; DB 164; Length 777; 50.6%; Pred No. 0 027;
                                                      0; Mismatches 152; Indols
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cultivar="Chinese Spring"
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/lab_host="E. coli SOLR"
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Location/Qualifiers
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                                                           Matches 156, Conservative
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Job time: 21891 sec

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greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the 3 Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491 aggtgatececatgtteaeegeeetyagegagggegeeaeeeeceaggaeetgaaeagga 550
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HYSMEHOUTH191 Hordonn voltage sendling root EST library HVcDNA0007 (cfiolated and unstressed) Hordonn vulgare cDNA clone HVSMEHOUTH191, mKNA sequence.

HF259495.2 G1:13120022 HF259495.2 G1:13120022 HS759495.2 G1:13120022 HS759495.2 G1:13120022 HS759495.2 G1:13120022 HS769495.2 G1:13120022 HS769495.2 G1:13120022 HS769495.2 G1:13120022 HS769495.2 G1:13120022 HS769495.2 G1:13120022 HS769495.2 G1:13120022 HS769495.2 G1:13120022 HS769495.2 G1:13120022 HS769495.2 HS76949695.2 HS769495.

J., Saski, C., Schwartzhock, J., Simmons, F., Choi, D.M., Main, D. and Wood, T. Development of a genetically and physically anchored EST resource for barley genomics Unpublished (2000) Onpublished (2000) On Nov 16, 2000 this sequence version replaced qi:lll88608. Contact: Wing RA Clemson University Genomics institute /note "Vector: lambdaZAF, Sile_1: EcoR1, Sile_2: Xhol" 282 c - 184 q = 133 t. 2 others 310 GACGAGGCAACCACGGCACCTTCGACTTCGTCTTCGTGGACGCCGACAAGACAACTAC 369 /clone_lib "Hordows unlgare seedling root war library HVCDNA5087 (ctiolated and unstressed)" 124 gagaagitiyqeetgaaceeeggeetqeiqaqaeeaqeeqaqqeetqeaaqeaqateate 183 73 CHCAACAFGCFGCFCAAGGFFCAFCGGCGCCAAGAAGAAGAFGAAGAFCGGCGFCFACAAGG 112 304. gastaagatidaagaagaagsaaaadaatgssaastaadaatssaqsaaqosqoon 363 364. gapangngcaaggitgagccanaactaccccateqtiqeanicctiqeniquqqqqcmqqitiqqtiq. 123 424. caccaqqccaftcaqcccccqcaccctuaacqcctqqqtqaaqqtqatcqaqqaqqcc-483 544 ctgaacacqatqttgaacaccqtqqqcqqccaccaqqccqccatqcaqatqctqaaqqac 603 184 egecagetycaereegecetgeagaeeggaagagagagaagtaaaaaareetgtteaacare 243 370 CTCAACTACCACGAGGGCCTCAIGAAGCTCGFCAAGGTCGGGGCCTCCTCGGCTACGAC 429 487 AFOCGCTACTACCGCGACTTCGTNCTCGACTTCAACAAGGCCCTCGCCGCGCGACCAGCGC 546 664 gedeceggenagatgegegageenegrygeagegaeategereggeaeneana 718 5.2%; Score 76.2, 48-146; Length 759; 47.7%; Pred; No. 0.00017; 47.7%; Pred; No. Mismatches 395, 104-18 6, Clemson Universitý 100 Jordan Hall, Clemson, SC 29634, USA /tissue_type="Seedling root" /lab_host:"TJC121" /organism."Hordeum vulgare" <u>-</u> Email, rwingsclenson.edu Seq primer: AATTAACCCTCACTAAAGGG /clone-"HVSME10019H191" High quality sequence stop: 757 /cultivar="Morex" /db_xret-"taxon:4513" Location/Qualifiers Conservation Fax: 864 656 4293 10cal Similarity . 8 Query Match source BASE COUNT Matches JOURNAL. FEATURES TITLE COMMENT OKICIN Ċ. 2 5 £ \ddot{o} £ $\tilde{\epsilon}$ <u>G</u> ŝ qq Ŝ g ô a ô

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Eukaryota; Viridiplantas, Streptophytu; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US Department of Agriculture, Agriculture Research Service, Pacific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoR]; Site_2: Xhoi; Plants were grown in the greenhouse Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and
                                                                                                                                                                                                                                                                                                                                                                                  Anderson, o.t., chao, s., choi.D w., Close, T.J., Fenton, B.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - pre-anthesis spike cDNA library
                                               HF4R4304 562 bp mPNA FST OA-DEC-2000 WHED311_FILLEX135S Wheat pro authesis spike PDNA library Tilticum aestivum cDNA clone WHED321_FI2_K23, mPNA sequence
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/clone_lib="Wheat pre-authesis spike cDNA library"
/tissuc_type="Spike before anthesis"
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50.4%; Pred. No. 0.00022;
tive 0, Mismatches 254, Indels 12,
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800 Buchanan Street, Albany, CA 94710, USA
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/db_xref="taxon:4565"
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/lab_host="E. coli SOLR"
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                                                                                  DEFINITION
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Wing, P., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: lambda2AP; Site_1: FroR1; Site_2: Xhol; For more details on libidity preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/" 245 c 272 q 71 t
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Spermatophyta: Magnoliophyta; Liliopsida, Poales; Poaceae; Pooldeae
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(20 DAE) HOEDEUm vulgare CENA clone HVSMEIGOZINZAE, MRNA sequence.
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422 igosocaggocatrayerringcaccetgaacgeetgggitgaaggitgategaggaggaagg 481
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/tissue_type="20 DAP spike"
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Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L., Tonq, J.C., Verhey, S.D. and Walker-Simmons, M.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HES17405 648 bp mkNA EST 08-AUG-2000 WHE0616,ALT,BLTCA WHE0616,ALT,BLTCA WHE0616,ALT,BLTCA WHE0616_ALT_BZ4, mkNA sequence.
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800 Buchanan Street, Albany, CA 94710, USA
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/note "Vector: pGAD10; Site.1: EcoR1; Site.2: Xhof;
Embryos were cut from mature, dormant seeds and imbibed in
25 microm ARA (abscisic acid) in 5 mM Mes buffer, pH 5.7,
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                                                                                                                                                                                                                                                                                                                                                                                                                      /cultivar "Brevor (soft, white, winter, common wheat)"
/db_xrel="taxon:4565"
/clone="WHE0616_A12_R24"
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                                                                Sequence have been trimmed to remove vector sequence and low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Wheat ABA-treated embryo coNA library"
/tissue_type "Seed embryo"
/dev_stage="Mature dormant seeds"
/lab_host "E. coli pH128"
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                                                                                                                    quality sequence with phred score less than 20 Seq primer: Clontech Matchmaker 3' AD primer.
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                                                                                                                                                                                                                                                                                                                                                                  /organism="Triticum aestivum"
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Email: oandersnapw.usda.gov
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betermination of this BAC-end sequence was carried out as part of a collaboration with the Herkely Diosophia Genome Froject (BDGF).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencaqe : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NY. The library is named ReL1-98 and was constructed by partial EcoRT digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or fillters for hybridization from the BACPAC Resource Center can be found at http://harpac.med huffalo.edu/drosophila_bac.htm.
Drosophila melanogaster genome survey sequence TET3 end of BAC # BACK19116 of RPC1-98 library from Drosophila melanogaster (fruit 11y), genomic survey sequence.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopteryyota; Diptera; Brachyera,
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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Wang/Bohnert lab"
/tissue_type="seedling"_
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/cultivar="B73"
                                                                                       Zea mays cDNA, mRNA sequence.
AI857214
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A1857214 595 bp
buguugbué,xl hu3 - stre
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Fax: 650 725 8221
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cDNA clone ZmO4_03q03, mKNA sequence.
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Single, A & Waken, K , Couroux, P., De Moors, A., Harris, L.J., Hattori
JJ.L. (amellet, T., Robert, L.S., Sprott, D. and Tinker, N.A.
Expressed Sequence Tays from Gold-Stressed Maize Seedlings
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                         219 CTACCECACCACCACCACCGCCTCCTGAACCTGGTGAGGCCGGCGGCGTCAFGGGCTA 160
                                                                                                                             Agriculture and Agri-Lood Canada
960 Carling Avenue, Bldg. 20, Ottawa, Ontario, K1A 0C6, Canada
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Matches 343; Conservative 14; Mismatches 443; Indels 6;
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Fax: (613) 759-1701
Email: singhja@em.ac
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Confact: Singh, LA
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Spermatophyta, Magneliophyta, Liliopsida, Poales, Poaceae, Pooldeae
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                                                                                                                                                                                                                                                                                                                                   CLASSUE_LYPE="Early reproductive apex"

/Lissue_LYPE="Seven week-old plants"
//dev_stage="Seven week-old plants"
//deb_nost== coll xinhs"
//deb_nost== coll xinhs"
//note="Vector: Lambda Uni ZAP XR, excised phagemid;
//note="Vector: Lambda Uni ZAP XR, excised phagemid;
//note="Vector: Lambda Uni ZAP XR, excised phagemid;
//note="Vector: Lambda Uni ZAP XR, excised phagemid;
//note="Vector: Lambda Uni ZAP XR, excised at the charter to flower state, a cDNA library was made, and the cDNA clones were in vivo excised at the University of California, Davis (V. Echemique, B. Stamova J. Dubcovsky). Plasmid DNA preparations and DNA sequencing were performed in the Ob Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       c i
                                                                                                                                                                                                                                                                                                 /clone_lib="Triticum monococcum early reproductive apex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 CICAACAAGGCCCTCGCCGCCACCAGCGCGCGGGAGATVIVVVAGAGTTAACAGGCGAGAC 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 ategigeagaactigeagggeeagatgigearraggraatragoeceegeaceigaac 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 gcctgggtgaaggtgatcgaggagaaggccttcagccccgaggtgatccccatgttcacc 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         514 gecetgagegagggggrannagennnagganetgaacaegatqttgaacaeeqtqqqqqqq 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          574 caucagguegeeatgeagatgetgaaggaeareatnaangagaaggnnynngagtgggan 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 CTCCCCCCACCCCCATGCCCAAGTACATCCCCTACTACGCGACTTCGTGCTCGAG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 ategaggteegegacaccaaggaggeettggacaagategagaggaggagcagaacaaqtge 333
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                                                                                                               sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20\, seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.7%; Score 69; DB 152; Length 509; Best Local Similarity 50.3%; Pred No 0.0035:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 215; Indels
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                  West Area, Western Regional Research Center
                                   800 Buchanan Street, Álbany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                        /organism="Triticum monococcum"
                                                                                                                                                                                                                                                            /db_xref="taxon:4568"
/clone="WHE2495_E11_I21"
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                                                                                                    Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                             /cultivar="DV92"
                                                                                                                                                                                                                                                                                                                           CDNA library"
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Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Bequm, D., Frisch, D., Yu, Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae;
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                        Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="HVSMED0089Colf"
/clone="HVSMED0089Colf"
/clone="Hordeum vulgare 5 45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP)"
/lisque_type="5-45 DAP Spike"
/lab_host="801k"
/note="Vector: lambda2AF; Sitc_1: ECOR1; Site_2: Xhol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lius eegaacaeeagaytyatyutyebgagageaaetteaagggeeeernggnynalegteaagt 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              983 gcdagaccallectgcgcqctcticggccccggcgagcctggagagafgafgargccf 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lambda2AF, Sitc_1: EcoR1; Site_2: Xho1"
11 g 130 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 TCTCCCGGGGGGGCGCTGCGGCGAGACAAGATCCTCAAGGTCATCCGCAAGAACCTCGTCA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 CCAAGCTCGCCCGACCTGCTCCCGTCCCACCAAGACGGCGCACGAGCTCACCAGCC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               803 tgaacaagatcylyggyalytacayccccylyydyculectygucalcuaydaagggceeea 862
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                                                                                                                                                                                                                                                                                                                                              on Jun žb, zoču this sequence version replaced gl-8707581.
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.04; Score 68.6; DB 164; Length 840;
44.38; Pred. No. 0.0042;
Live 0; Mismatches 349; Indels 0;
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/rione_lib-"Mastigamoeba balamuthi lambda ZAP II Library"/note-"syn: Phreatamoeba balamuthi"
516 c 443 q 204 t
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                                                                                                                                            1283 united gaycaaqatetqqeeeaqeeaaqqeeqeeeqeeeqeeeacttectqeaqqee 1342
                                                                                                                                                                                                                             1223 getget gaugt im genaagga (genoanzez jan gan geni goassgage proaggeta (1282
                                                                                   rocketeller.0.370 Mastigamodba balamuthi iambda DAF II Library
Mastigamodba balamuthi cDNA similar to pyrophosphater-fructose
6 phosphate l-phosphotransforase, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 TCARGOACHACOLCACCOGGA TGARGACAGAGACACATCTACTACATCACCGGCG 443
                                                                                                                                                                                                                                                                     393. catogi qilaqaacctqcaqqqccagatgqtqcaccaqqccatcaqcccccqcccqqaa. 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    513 egeretigaggaggegeracececaggaget gaacagatgttgaacacegttgggegg 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA clones (expressed sequence tags) from the free-living amifochondriate amocboflagellate, Mastigamocba balamuthi
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43.8%; Pred. No. 0.0061;
Live 0; Mismatches 512; Indels 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fle Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller-frockvax.rockefeller.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Muller Miklos
Laboratory of Biochemical Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                 1103 uqaaqoaqqaabqoaqqaaqa 1429
                                                                                                                                                                                                                                                                                                                                    /strain "ATCC 30984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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1 (bases 1 to 1427)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1427 bp
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; Triticeae; Hordeum.
1 (bases 1 to 770)
Wing,R., Close,T.J., Kleinhots,A., Wise,R., Hequm,D., Frisch,D., Yu
Wing,R., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE193183 770 bp mkNA ESI 02-MAK-2001
HVSMEh00080R02f Hordcum vulgare 5-45 DAP spike EST library
HVcDNAQ009 (5 to 45 DAP) Hordcum vulgare chNA clone HVSMEh0080Bu21,
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                   /clone_lib="Hordeum vulgare 5:45 DAP spike EST library
HVCDNAQ009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                              /note="Vector: lambdazAP, Site_1. EcoR1, Site_2. Ahol"
226 c 247 g 115 t 3 others
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Impublished (2000)
On Jun 26, 2000 this sequence version replaced 91:8705362.
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.5%; Score bo.z; UB 164; Length 770; Best Local Similarity 47.3%; Pred. No. 0.012; Matches 274, Conservative 6; Mishatches 293, indels 12;
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Tel: 864 656 7288
Fax: 864 656 4293
                          Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                               /organism="Hordeum vulgare"
                                                                                                                                                                                                                          /db_xref="taxon:4513"
/clone="HVSMEh0080B021"
                                                                                                                                   Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                   High quality sequence stop: 659.
Location/Qualifiers
                                                                                                                                                                                                            /cultivar="Morex"
                                                                                                                        Email: rwing@clemson.edu
                                                                                                                                                                                      source
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RESULT 12 AV391237

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Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Fana 1532-3, grakannakasusa or.jp. UPL-brtp://www.kazusa or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                       Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 599)
Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
A large scale structural analysis of cDNAs in a unicellular green alga, Chlamydomonas reinhardii. I. Generation of 3433
non-redundant expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib-"Chiamydomenas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/no+e="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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               AV 91237 Chlamydomodas reinhaidtii 79 Chlamydomonas reinhardtii
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4 5%; Score 66; DB 30; Tenath 599;
Best Local Similarity 47.8%; Pred. No. 0.012;
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0; Mismatches 210; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Chlamydomonas reinhardtii"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                   CDNA clone CMUbycul_r, mkNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="+axon-3055"
/clone="CM069c07_r"
       mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 g
                                                                                                                                                                                                                                                                                                                                                                                                                            Yasukazu Nakamura
                                                                                                                                                 Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
                                                                             AV391237
AV391237.1 GI:6545453
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     299 bp
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  AV391237
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Eukaryota; Viridiplantao; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lilliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mote-"Vertor: pGAD10; Site_1: EcoR1; Site_2: Xho1; Embryos were cut from mature, dormant seeds and imbibed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAN were prepared by Steach Verbey in M.K. Walkers's simple as a de CBSA ARS, Washington State Univ., Pullman, Washington GGL44-6420. A CDNA library was made by Clontech using a combination of random and oligo dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primers. Library was plated and archived by Russell Johnson (Colby College, MF/Walker Simmons' lab.) Plasmir DNA preparations and DNA sequencing were performed in the Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                              Anderson, O.D., Chao, S., Han, P.S., Hsta, C.C., Johnson, R.R., Kand, Y., Lazo, G.W., Miller, Ransel, C.J., Seaton, C.L., Tong, J.C., Verhey, S.D., and Walker-Simmons, M.K.
The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          deroM ABA (abscisic acid) in 5 mM Mes buffer, pH 5. 12 hr at 22 \%. The tissue, total RNA, and poly(A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar-"Brovor (soft, white, winter, common wheat)"
/db_xref "taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 notigtantigngtignangagagabnyaggtinngegannaaggagaggagagat 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 i aaygtigayii ayaartariiis atriytyi agaaniityraqqqiinagatygtycaccaggo (431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Clontech Matchmaker 3' AD primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="WHEG615_F02_L03"
/clone_lib="Whoat ARA-treated embryo_cDNA_library"
/tissue_type="Seed embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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destivum cDNA clone WHEO615_F02_L03, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage."Mature dormant seeds"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Oandersn4pw.usda.gov
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                                                                                                                                                                                                                                           Triticeae; Triticum.
1 (bases 1 to 627)
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Best Local Similarity 45.6%;
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                            ACCESSION
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1 275 c 199 q 97 t 5 others
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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Corronsatz 3, D 06466 Gatersleben, Germany
Email: michait K Fight datersleben, de, http://par.ipk-qatersleben.de
Seq primer: T3 primer for 5'end.
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492 igaggitgatioeoralgitikacogoorigagogaggggggggggggggggggggggggg 551
                                                                                                                                                                                                                                                                                                                                                                                         352 geogaggregeegaraagggeaaggtgageeagaartaereerategtgtgagaeetgeag 411
                                                                                                                                     432 cut eageconegeuscottalangonlyqqtqaaqqtqaateqaaqaaqaaqqont tidaqoo 491
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AL507813
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44.7%, Pred. No. 0.019;
Live 0; Mismatches 349; Indels
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Contact: Michalek W
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1 (bases 1 to 700)
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Mammalia; Butheria; Primates; Catarihini; Hominidae; Homo.
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29 GOOGANGOOGGOOGGOOGGAATGGACTGGGTGGGGGTGGTGGGGGGCTGACGCCGNTG 88
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BP 191 91006 EVRY redex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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and cloned into the Not I and Eco RV sites of the pcMVSPORI 6 vector. Library was constructed by Life Technologies. Context: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville. Maryland 20850, USA Fax : (1) 301 610 8371 Email :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AF201927 Synthetic	AF287354 Synthetic	AF202464 Synthetic	AF202465 Synthetic	AP287352 Synthetic	AF287353 Synthetic	AX0454 Sequence	AX056836 Sequence
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6) PERINGERI VARARARARARARA BARARA TOAMARA YARAKOTISTARARA MAGOOOARA
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Best Local Similarity 88.5%, Fied No. 3.2e 3.2.
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/db_xret="G1:7248703"
/product-"gad protein"
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Submitted (12-JUL-2000) Chemical Pathology, Women's and Children's Hospital, 72 King William Road, North Adelaide, SA 5006, Australia Location/Qualifiers
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Included explosion and immunogenicity of sequence-modified human immunodeficiency virus type 1 gag gene
1 Virol 74 (6), 2628-2635 (2000)
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/product="qag-protease fusion protein GP1"
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/db_xref "G1:7229425"
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0, Mismatches 192; Indels
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/db_xref="taxon:32630"
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Street, Emeryville, CA 94608, USA
Location/Qualifiers
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Direct Submission
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Matches 1299, Conservative
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526- genammengagammaaanamatat taaamamat gadagamaagamaagamaagamaga 585
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KTEEGUNESEKKRAQQAAAAAGTGNSSQVSQNYFTVQNT©GMVHQATSPFTLNAWVKV
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KCPNOGKEGHTARNCPAPRKGGWPOSPEGHOMKNOTFPGANFLGRÜMPSYKGRPGNF
LUSBOPOFAPPPESERPCFEKT FESGKGEFIDKELYPLI SLASLFGNDFSSQ"
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RMYSPTSTLGTEGGPKEPFRDYDREYKTLKAEGASQDVKNWMTETLLVONANPPKKT
Synthetic construct gag professe fusion profein GP2 gene, complete
                                                                                                                                                                                                                                        Increased expression and immunogenicity of sequence-modified human
                                                                                                                                                                                                                                                                                                                                                                                                                  Chiron Corporation, 4560 Borton
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Selby,M., otten,G R. and Harnett,S.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity 85.1%; Score 1117.8; DB 56; Length 1847; Similarity 85.1%; Pred. No. 3.1e-113; Observative 0; Mismatches 192; Indels 46; C
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/protein_id="AAF42829.1"
/db_kret-"GL:7229427"
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                                                                                                                                                artificial sequence.
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/translation="REDLAGE ARKESSEQTEANSF!PREFQVWFPDNNSTSFAGA PROGRAVSFSPPOTITUMGPPLVTIKTGGGLKEALLDTGADDTYLEEMIEPGKKKPKMIG GIGGFIKVGYDQIPTEICGHKA!GTYLVGFTFVNILGKNLLYGIGJENFFYBFBIET VPVKIKFGWROCFVKOWPTTEFKIKALVEICTEFREKKAFFKEKTSKIGPENPYNTPVFAIKK KUSTRWFRLYDFPERIKFTAFFTIKFTIFFKIKAFFQFWFAIKF KUSTRWFRLYDFPERIKFTAFFTIKFTTFFYGTFWFVGTGTPHPAGLKKKSYTYLVJGGAYFSVPLHED FFYTAFTIFSTNNFTFPGTFYGYNVLPQGWKGSPAIFQSSMTTILEPFKKGNPDLVIY
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EAELBELAENKEILKEPVHGVYYDPSKOLJAEJŲKOGOSŲMIYOJIYŲEPEKNIKTGKYA
PĮRGAHTNIPVKOJI TEAVQKIATESIVIMGKIPKFKLPIQKETWETWITEYWOATWIPE
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TTNOKTELQAIYLAQOSGLEVNIVTDSQYALGI IQAOPDRSESELVSOI IEQLIKKE
KVYLAWVPAHKGIGGNEQVDKI.VSAGIRKVLFLDGIDKAQEEHEKYHSNWRAMASDFN
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NPGSGOOVVESMNKELKKTTGOVPPGAEHLKTAVQMAVETHNEKRKGGIGGYSAGERIV
DIIATDIQTKELQKOITKIQNEPVYYPPSRPPIWKGPAKILWKGRGAVVIQDNSDIKV
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Avppilienseggegilgolgoslongseelpslynnvatlycvhokievkdkeale
Kiebeonkskkkagoaaadtonssovsonypivonlongoaisppinonypinon
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KALGPAATLEEMMIACGGVGGPCHKAKVLAEAMSQVINSALIMMCHGNFFNGFRIVKC
FNCCKECHTAKNCPAPPKKGCWFCGKEGHQMKIKTTERGANFLGKIWPSHKGRPGNFLQ
SRPEPTAPSEESVRFGEETTTPSQKQEPIDKELYPLASLRSLFGSDFSSQ"
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Fuller,M. and Anson,D.S.
Direct Submission
Submitted (12-JUL-2009) Chemical Pathology, Women's and Children's
Hospital, 72 King William Road, North Adelaide, SA 5006, Australia
Location/Oualifiers
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/db_xref="taxon:32630"
/nore-"derived from Human immunodeficiency virus type l
1423 ICPCAGAAGCAGGGGGGATAGAGAAGGAAAGTGTATGAGTTGGTTTGAGTCAGATCACTC 1482
                                                                                                                                                                                                                                                                                                 Synthetic construct HIV-1-derived gag protein and pol protein
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/db_xref="GI-11066863"
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/product="gag protein"
/protein_id="AAG28735.1"
/db_xref="G1:11066862"
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                                                                                                1483 TTTGGCAACGACCCTCGTCACAGTAA 1509
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Direct Submission property of Chemical Patheloay, Women's and Children's Sprintited (12-JUL-2000) Chemical Patheloay, Women's and Children's Hospital, 72 King William Road, North Adelaide, SA 5006, Australia
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GAANKETKLGKAGYYTNKGKČKVVSLTGTTNQKIELQAIYLALQGSGLEVNIVTDSQY
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LFLDGIDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCQLKGEAMHGAVCUS
PGIWQLDCTHLEGKVILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVTTIHT
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TAVOMAVFIHNFKRKGGIGGYSAGEPIVDIIATDIQTKELQKQITKIONFKYYYRDSR
DPLWKGPAKLLWKGEGAVVIQDNSDIKVVPRFKAKIIRDYGKÇMAGD/XYAGKÇÜED"
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KTEEEQNKSKKKAQQAAAD1GNSSQVSQNYP1VQNLGGGWYHQAISPRTLNAWVKVVE
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YSPTSILDIPOGPKEPFPPYVDRFYKTLRAEGASGEVKNWMTETTLVQNANPDCKTIL
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| HIIIII | HIIIIIIII | HIIIIIII | HIIIIII
| TACAAGGAAAGGCAAGGAACHTTCTTCAGAGCAG
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Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
1 (bases 1 to 4307)
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Anti-Viral vectors

Anti-Viral vectors

Anti-Viral vectors

MIROPHANOUS KRIAGOS (GB); KINGSMAN ALAN JOHN (GB), OXFORD

BIOMEDICA LTD (GB); KIM NARRY (KR)
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Best Local Similarity 77 7%; Pred. No. 5.5e 93;
Matches 1173; Conservative 0; Mismatches 506; Indels 30;
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/db_xref-"taxon:12721"
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AX019132 G:: 10043165
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/db_xref="taxon:32630"
/note "psYNni94 - codon optimised HIV-1 qaqpol with 20 bp
of the leader sequence of HIV-1, etc"
1 1194 c 1296 q 693 t
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1 (bases 1 to 4327)
Uden,M. and Mitrophanous,K.
Anti-viral vectors
Patent: WO 0055341-A 14 21-SEP-2000;
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AX035465
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592 cigaaggaeeacatraangaggaggrngrngagtggaeeqeetqeaceceqiqeaqqee 651
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/organism="synthetic construct"
/db_xret "taxen: 42630"
/db_xret "taxen: 42630"
/noie="psyNGP3 - codon optimised HIV-1 gagpol with leader sequence from the major splice donor"
a 1198 c 1302 q 700 t.
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Fatent: Wo 6055341-A 13 21-SEV-2000;
UDEN MARK (GB) : OXFORD RIOMEDICA LTD (GB) ; MITROPHANOUS KYPIACOS
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Sequence 13 from Fatent W00055341
AX035464
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1489 agegyeeveetyayeeagtaa 1509
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Matches 1175; Conservative
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Sequence 12 from Patent W00055341. AX035463

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    4642
        //organism="synthetic construct" //db.erel="Laxon:326.0" //db.erel="Laxon:326.0" //db.erel="laxon:326.0" //db.erel="laxon:326.0"
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0; Mismatches 316; Indels
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GPGAILEEMMTACOGYGGFGIKARVIABAMSOANSVNIMMOKSNEKGPPRNVKFFNCG
KEGHIAKNCRAPRKKGCWKCGKFGHQMKDCTERQANFIGKIMPSHKGRPGNFLONRSB
PAAPTVPTAFPAESPREETTTPAPKQEPKNFEPYREPLIALRSIFGSGPLSQ"
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LKWGFTTPDKKHGKBPPFLWMGYELHPDKWTVQPIQLPDKDSWTVNDIQKLVGKLNWA
SQIYPGIKVKGLCKLLRGARALTDVVPLTEBAELELAENRFILKEPVHGYYPDFSKDL
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LKTAYQMAVETHNFKRKGGIGGYSAGERIIDIIATDIQTKELQKQIIKIQNFKYYKD
SRDPIWKGPAKLLWKGEGAVVIQDNSDIKVVPRKKAKIIKDYGKQMAGADCVAGGODE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"mgarastirgerinkwertrippgekkhywikhi.wwasrelegf
Alnpglietargckojmkolopalotgteelkslyntvatlycvhagievrdykald
Kieeegnksqoktogakeadgkvsonypivonloggwyhqaisprtlnawykvieeka
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ASSENSTNSPPSREDÇVPGDNPPSERATARGGCFLQGTLNCPQITLWQRPLVSIKVGGQ
IKEALLDTGADNTVLEEINLPGKWKPKMIGGIGGFIKVRQYDQIVIFICGKKAIGTVL
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EICEEMEKECKITKI GPENPYNTPVPAIKKKDSTKWKKLVDFKELNKKI ULFWEVULG
IPHPAGLKKKKSVTVLDMGDAYFSVPLDEGFRKYTAFTIPSINNETPGIRYOYNVLPO
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KMLPLDGI DYRAQREHPKYHNNWRAMADEFNLPPI VAKETVASCDKOQLKGFA I HGQVD</u>
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GPGATLEEMMTACQGVGGPGHKARVLAFAMSQANSVNIMMQKSNFKGFRRNVKGFNCG
                                                                                                                                                                                                                                                                           Submitted (03-DEC-1998) Immunology and Infectious Diseases, Harvard School of Public Health, FXB-310, 651 Huntington Avenue, Boston, MA
                                                                                                                                                          2 (bases 1 to 9056)
Novitsky,V.A., Montano,M.A., McLane,M.F., Renjifo,B., Vannberg,F.,
Foley,B.T., Ndung'u,T.P., Marlink,R. and Essex,M.
Immunodeficiency virus type 1 subtype C a set of 23 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Human immunodeficiency virus type 1"
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/protein_id="AAD17071.1"
                                                                J Virol 73 (5), 4427-4432 (1999)
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/db_xret="G1:4324808"
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/note="subtype: C"
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277. . 45на
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AS_zret="Gi.4 K24814"
/transid-ation "AK24814"
KEAKITLECISIAKAYEEEVHNVWATHAZYPIDHIQEIVLENVTENVMWENDAUGO
                                                                                                                      ESKRIKVSSEVH I PLOGRAFI V LKTYWILOTOFPOWIHOGHSV EWROPKYSTOVEPOL.
ALGOLTHMIYPEUGEAGAAL HAA I LOSTEV VYDANIHOGVESLOFIALI ALLI REKOPK
PPLOSVYKLVEDRAWKEOKTEVIPONITMANI"
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YVYETYGDIWIGVETLI PLIQQI LETHEPIGOGESPIGIL PQPPTFNRASPS"
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Wrakgkgihslisfpttsattgepaepvegtpptlekihtle"skswitsgtpgvp"
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DRUTKKIRERAEDSONESDGDTEELSAMVDVGHIRLIDVNN"
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DREINNYTDTIYRLLEESGNQGEKNEKBLILALDSWQNLWNWFSITNWLWYIKIFIMIV
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LVSGELALAMDGLRSTTLESYHRLRDPTLTAARVLFLLGGRGWPATRYTGSLVQYWGT
                                                                                            /translation-"MENRWQVLIVWQVDRMKIRTWNSLVKHHMHISKRAKGWFYRHHY
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/qene="rev"
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Agenr="tat"
                                              /profein_id="AAD17073.1"
/db_xref="G1:4324809"
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/db_xref "G1:4324810"
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/db_xref="G1:4324812"
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/codon_start-l/product="Vil"
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/qetter "env"
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/4080 "YEL"
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/qene-"vpu"
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/qene="rev"
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PUBMED REFERENCE AUTHORS	TITLE JOURNAL	FEATURES sou		LTR gene	gene	CDS	gene	CDS	gene		aebe	CDS	gene		dene	SOD	
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VSILDIROGPKEPFRDYVDRFFKTIRAROATODVKNWMTDYLLVONNPDCKYILLRAL
ORATILEBMYARCOGYGGPSKRAVLIARAROATSTNILMORSNFKGPRYVKCFNCG
KEGHIARNCPAPRKGZWKYSPRSHOMKOYTERGANFLKTWRGPKYRGPROFP
TAPPAAEPTAPPAESFRFEGTIPAPKQEPKDREPLISLKKSLFGNDFLFQ"
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PLDEGFRKYTAFTIPSTNNETPGIRYOYNVLPOGWKGSPAIFOSSMTKILEPFRIQNP
GIVIYOYMDDLYVGSDLEIGQHRAKVFELREHLLKWGFTTPDKKHOKEPPFLMMGYEL
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alnpslletadgckqiirqlhpalqtgteelrslentvatlycvhaeidvrdtkeald
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PRSETGAERQCTLNLPQIALWQRPLVSIKVGGQVKEALLDTGADDTVLEEINLPGKWK
PKMIGGIGGFIKVRQYDQIPIFICGKKALGTVLVGPTPVNIIGRNMLTQLGCTLNFPI
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Birmingham, 701 19th Street, South, LHRB 641, Birmingham, AL 35291,
                                                                                                                                                                                                                                                                                                                                                                                                           lentivirus group.
1 (bases 1 to 9034)
Podenburg, M . Li, Y , Trask,S.A., Chen,Y., Decker,J.,
Podentson,D.I. , Kalish,M I., Shaw,G.M., Allen,S., Hahn,B.H. and
              1717 AGGGAACCCTAAAAGGAAACCCTTAACTGCCCTCAGATCACTCTTTGGCAGCGGCCCTTG 1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vear full-length clones and reference sequences for subtype C isolates of HIV type 1 from three different continents AIDS Res. Hum. Retroviruses 17 (2), 161-168 (2001)
                                                                                                                                                                                                                       10.AFR:2001
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Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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                                                                                                                                                                                                                       AF286234 9034 bp DNA VRL 1C
HIV-1 strain 98T2013 from Tanzania, complete genome.
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/protein_id="AAK31054.1"
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ADQLIHMHYFDGFADSAIRKAILGHIVIPRCDYQAGHNKVGSLQYLALTALIKPKRRK
PPLPSVRKLVEDRWNNPQKTRGRRGNHTMSGH"
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                                                                                        ITLAETTNQKAELQAIOLALQDSGSKVNIATDSQYALGIIQAQPDKSESELVSQIÎEQ
LIGKERVYLSWYPAHKGIGGNEQVDKLVSSGIRKVLFLDGIDKAQEEHEKYHSNWRAM
ASEFNLPPIVAKEIVASCDKCQLKGEAIHGQVDCSPGIWQLDCTHLEGKIILVAVHVA
SGYIEAEVIPAFTGQETA"
VPLIKEAELELLEENKETTKEPVHGVYYDPSKDLIAETUKGGGDOWTYQTYQEPFKNLK
TGKYAKMRSAHTNDVKQLTEATQKTAMESTVIWGKTPKFRLPTQKETWETWWTDYWQA
                                                             TWI PEWEFVNTFPLVKEWYQLEKEL IAGAETYYVDGAANRESKI GKAGY ITDRGRQÄI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(5312. .5387,7733. .7980)
/gene="rev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(5173. .5387,7733. .7823)
/gene="tat"
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/protein_id="AAK31059.1"
/db_xref="GI:13569324"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="vpr protein"
/protein_id="AAK31056.1"
/db_xref-"Gi:13569321"
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                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAK31055.1"
/db_xref="G1:13569320"
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/product="rev protein"
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AKYGAFTI SNIVATNADI AMILBAQEBERENGEPVRPQVPI RPMTYRAAPNI SFETKER
GGLEGLITYSKKRODILLDIMVYHTQGFPRDMONYTPGPGVRYPLTFGWCFKLVPVDPRE
VEEANKGENNYT I HPMSQHGMEDGFPVLAMEFDSSI ARPHILADEKHPEYYEGO."
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HYCTPAGYATLKONNKTENGTOPCKNVSTVQOTHGTKPVVSTQLTTNGSLAFFTVTR
                                                      SENITONAKT FIVHINESVETMCTRPGNNTRKSVRIGPGQTFYTNDTIGDIRQAYONI

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                          856_CAGGAACAAATAGCATGGATGACAGGTAACCCACTGTTCCAGTGGGAGACATCTATAAA
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Gandore version 4.5
Copyright (c) 1994 - 2000 Compuges Itd
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Addust 8, 2001, 18:25:61; Scarch time 252.53 Seconds (without alignments) 3677.450 Million cell updates/sec Run cn:

US-09-475-704-3 1479 Title: Perfect secret

..angannoncigagenaqtaa 1479 1 at gggggggggggggggtgt Sequentions

Gapop 10.0 , Gapext 1.0 Scoring table:

730101 seqs, 313950809 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Listing first 45 summaries

Database :

/cgn1_9/gcudata/deneseq/geneseqn/NN1993.DAT:*/cgn1_9/gcudata/deneseq/deneseqn/NN1994.DAT:*/cqn1_9/gcqdata/qeneseq/qeneseqn/NN1995_DAT:* /cdn1_9/dcqdata/qeneseq/qeneseqn/NA1996_DAT:*
/cqn1_g-dcqqdata/qeneseq/qeneseqn/NA1996_TAT:*
/cqn1_g-dcqdata/qeneseq/qeneseqn/NA1998_DAT:*
/cqn1_g-d-qqqdata/qeneseq/qeneseqn/NA1998_DAT:* /cqni_9/4cqdata/qcncscq/qcncscqu/NAi987.DAf;*/cqni_9/4cqdata/qcncscq/qcncscqn/Nai988.DAT;*/cqni_9/4cqdata/qcnescqy/qenescqn/NAi989.DAT;* /cgnl_9/gcgdata/geneseg/genesegn/NA1990.DAT:* /cgsl_9/gcgdata/geneseg/genesegn/NA1991.nAT:* /cgsl_9/gcgdata/geneseg/genesegn/NA1992.DAT.* /cqnl_9/qcqdata/geneseq/qeneseqn/NN1984.DAT:*/cqnl_9/qcqdata/qeneseq/qeneseqn/NN1985.DAT:*/cqnl_9/qcqdata/qeneseq/qeneseqn/NN1986.DAT:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the fotal score distribution.

9.7qcgdata/qrmeseqj/qemeseqtg/NA2606_1AT_.* /cgnl_9/qcqdata/geneseq/geneseqn/NA2001.DAT:*

SUMMARIES

a	etic Gau	optimize	HIV synthetic Gag	cptimise	HIV Gaq	HIV bicistronic co	tronic co	tronic co	HIV bicistronic co	HIV Gag/	AIV Cautenroteago
Description	HIV synthetic Gaq	HIV codor.	HIV Synth	HIV codon	Synthetic	HIV bicis	HIV bicis	HIV bicis	HIV bicis	Synthetic	HIV Cau-n
9	AAA51609	AAA51625	AAA51610	AAA51626	AAA70412	AAA70472	AAA70473	AAA70471	AAA76470	AAA70415	AAA70413
Ŧ.	21	[7.1	<u>-</u>	21	<u>.</u>	2.1	7.	21	2.1	5
Ouery re Match Length DB 1D	1479										
Ouery Match	100.0	5.85	100						0.18		
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BIV Gag-profedse e	HIV Gag-protease e	HIV Gad-polymerase	Codon optimised Hu	Packaging construc	HIV Gag common reg	Humanised EIV-1 qa	Synthetic FIV gag	HIV gagpol -SYNgp C	Human immunodefici	Nucleotide sequenc	HIV partial leader	HIV partial leader	HIV complete leade	Humanised HIV-1 qa	HIV-1 non-subtype	HIV-1 non-subtype	BIV-1 non-subtype	HIV-1 non-subtype	Complete sequence	Entire sequence of	HIV: 1 non-subtype	HIV-1-JC intection	HIV-1 non-subtype	HIV-1 non-subtype	HIV wild type gagp	Bultan influenced ici	Nucleofide sequenc	Human immunodetici	Attenuated HIV-1 s	Sequence of LAV vi	pHIV32 tragment co	Insert region of v	Insert region of v
AAA70475	AAA70476	AAA70414	AA252051	AAZ52055	AAA70417	AAF 4128 4	AAV45173	AA208740	AAA93972	AAC86876	AAA93984	AAA93983	AAA93982	AAF31286	AAF57929	AAP57926	AAPS7922	AAF57927	AAQ066.45	AAN80436	AAF57921	AAX03986	AAF57919	AAF57923	AA208722	AAA+3471	AAC86875	AAF24377	AAT14180	AAN60365	AAT04701	AAV+0.25.2	AAV58244
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75.4	75.4	1	71.7	71.7	69.3	0.99	65.9	64.2	64.2	64.2	63.5	67.59	in 7.3	63.1	50.0	49.3	48.1	47.4	45.3	7.1	44.6	44.6	44.5	44.4	44.0	ु · ₹*	44.0	0.44	44.0	5 5 7	43 7	44.7	43.7
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ALIGNMENTS

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AAA51609 standard, DNA; 1479 BP.
             (tirst entry)
             31-OCT-2000
         AAA51609;
  AAA51609
RESULT
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Sag, expression cassette, antiquaie, type C. HIV, Env. synthetic; DNA immunization, packaging cell line; antigen presentation, ss.

HIV synthetic Gag polynucleotide.

Human immunodeficiency virus type C strain AF110965. Synthetic.

/product. Synthetic_Gaq /note= "Codon usage pattern was modified and inhibitory elements (INS) and RRE sites were inactivated resulting in improved expression" Location/Qualitiers ซ .1479 /*t.ag =

W0200019304 - A2.

99WO-US31273. 30 DEC 1999; 06 JUL 2000.

99US 0152195. 31-DEC-1998; 01 SEP 1999;

98US-0114495.

(CHIR) CHIRON CORP.

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Expression cassettes comprising a polynucleotide encoding autigenic type C human immunodeficiency virus (HIV) Gag or Env polypeptides are useful in DNA immunization, generation of packaging cell lines and production of Gag- and/or Env-containing proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of cytotoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antigen entrapped or associated to the immune system of the host.
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                                                                                                    Polynucleotide encoding antiqunic type C HIV Gug polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal
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                                                                                                                                                                                Claim 2; Page 92-93; 113pp; English.
                                                                                                                                             especially human against HIV
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               Zur Megede J;
                                                   WPI; 2000-452401/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                    P-PSDB; AAY96943.
               Barnett S,
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66) arryroccogoccagatacacgagccocqcggcagcgacatcgccagccagcaccagcacc
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                                        bbl atogeceeeggeeagatyegeqqqqennynygnagnyanatngneggeacee
                                                                            721 etgeuggageagategeetggatgaeeageaannnnnnatnnngtgggnganatetae
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0; Mismatches 10;
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W0200039304 AZ.
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Expression cassettes comprising a polynuciectide encoding antigenic type C human immunodeficiency virus (HIV) Gaq or Env polypeptides are useful in DNA immunization, generation of packaging cell lines and production of Gag- and/or Env-containing proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of cytocoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antigen entrapped or associated to the immune system of the host.
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                                                                                                                                    DNA immunization; packaging cell line; antigen presentation, SS.
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                                                                                                                                                                                                Human immunodeficiency virus type C strain AF110967.
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                          HIV synthetic Gag polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production of Gag- and/or Env-containing proteins. Synthetic Env and Gag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucheotide encoding antigenic type C HIV dag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV
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                                                                                                                                                                                                                                                                                                                                                                                       DNA immunization; packaging cell line; antigen presentation; ss.
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                                                                                                                                                                                                                                                                                                                HIV codon-optimized synthetic Gag polynucleotide.
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                                                                                                                                                                  AAA51626 standard; DNA; 1509 BP
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                                                                                                241 accordocaccetigtaetigegtigeaegeeggeategaggtigegegaeaeeaaggaggee
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The present sequence is the coding sequence of a HIV Gag expression cassette, Gag.ModSF2. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV
                                                1258 paggartgraccqagngrraggrraacttrrtgggcaaqatctqqcccaqccacaaqqqc 1317
                             1378 ecececycegagagetteegettegagagaecaceeeegeeeeageagageeeaag 1437
                                                                                                                                                1420 g------acegegagaecetgaecagectgaagtettgatetgtteggeaaegaeee 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu H;
                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic HIV Gag expression cassette coding sequence Gag.ModSF2.
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slby M, Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection and acquired immunodeficiency syndrome (AIDS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV-1; AIDS; Gag; vaccine; expression cassette; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                 AAA70412 standard; DNA; 1515 BP.
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81.0%; Score 1197.8; DB 21; Length 1515; 89.3%; Pr-d. No. 3 5-756;

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1009 eccygoycoaycetygagagatgatgatcgcctgccaggggtgggggggggcccagccac 1068
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bl ctgcgccccygcygcaayaaytyctacatyatyaagcacctggtgtgggccagccgagg
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The present invention relates to synthetic HIV Gag and Env expression cassettes. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many states of the HIV life eyele, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The
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1087 aaqqeecqeqtqetqqeeqaqgeqatqaqeeaqqtqaeqaaeeeggegaeeateatgatg 1146
                              1147 caqoqoqqoaacttocqcaaccaqoqgaaqaccqfoaaqfqoffoactgoqqcaaqqaq 1206
                                                                                            1207 gyccharamgenaygaactgemyegeeneegeagaagaggetgetgegetgeggeege 1266
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                                                                                                                                                                                                                                        Expression cassettes encoding the human immunodeficiency virus
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                                                                                                             Lian Y,
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iby M, Walker C;
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Gag- and Env-polypeptides which may then be used to vaccinate against HIV
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                                                                     infection and acquired immunodeficiency syndrome (AIDS). The present sequence is a synthetic construct constructed in the generation of the
expression cassettes may be used for the recombinant expression of HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1197.8, DR 21, Lonath 4472;
Pred. No. 3e-150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Internal Ribosome Entry Site (IRES) is present.
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Best Local Similarity
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              3779 comercagnationings and troyous aggineria aggagement incanga antanataga of 3838
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                                             889 egettetteaagaeeetgegegeegageageageaeeeeaggaggtgaagaaetggatgaee
HIV bicistronic construct gp160.modSF162.drlV2 Gag mrdSF2.
                                                                                                                    HIV-1; AIDS; Gag; vaccine; expression cassette;
                                                                                                                                                                                                                          1069 aaggeeegegideiggeegaggeegalgageeaggeeaa
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   Chimeric - Cytomegalovirus
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The present invention relates to synthetic HIV Gag and Env expression cassettes. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassettes may be used for the recombinant expression of HIV
                                                                                                                                                                                                                                                                                                                                                                                      Gag- and Env-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (ALDS). The present sequence is a synthetic construct constructed in the generation of the persent invention. This construct is bicistronic in that the coding sequences for Env and Gag are under the control of a single CMV promoter and between the two coding sequences an Internal Ribosome Entry Site (IRES) is present.
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cassettes. The day protein of HV is needed for the assembly of virus-like particles. In addition, the day protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassettes may be used for the recombinant expression of HIV day—and Env-polypeptides which may then be used to vaccinate against HIV infection and acquired immandaticiery syndrome (ALES). The present sequence is a synthetic constructed in the generation of the
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                                                                                                                                                                                                                                                                                                                                                                                            , Zur Megede J, Srivastava I, Lian Y, Hartog K, Selby M, Walker C;
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HIV bicistronic construct gp160.modUSF162.Gag.modSF2.
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Chimeric – Human immunodeliciency virus type 1.
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cassettes. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassettes may be used for the recombinant expression of HIV cast and Euv-pulypetitaes which may then be used to vaccinate against HIV infertion and acquired immunodeficiency syndrome (AIDS). The present sequence is a synthetic construct constructed in the generation of the pricing of the present invention. This construct is blicistronic in that the coding sequences for Env and Gag are under the control of a single CMV promoter and between the two coding sequences an internal Ribosome Entry Site (IRES) is present.
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                                      61 ctgcgccccggcggcaagaagtgctacatgatgaagcacctggtggggccagcgcgg 120 [[[[[[[[]]]]]]]]]
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The present sequence is a HIV Gaq/Hepatitis C virus (HCV) core fusion coding sequence. The Gaq protein of HIV is needed for the assembly of virus-like particles. In addition, the Gaq protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The present invention relates to synthetic HIV Gaq expression cassettes. The present sequence was cloned and used to generate the expression cassettes of the present invention. The expression cassettes may be used for the recombinant expression of HIV Gaq-polypeptides which may then be used to vaccinate against HIV infection and acquired imminodefliciency syndrome
4433 gyocanaccyccaqqaactqrcgcgccccccqcaagaaqqqctqctgqcqctqcqqccqc 4492
                                                                     1243 gagggeeaecugatgaaggaetgeaeegagegeeagggeeaartteetgggaagetetgg 1302
                                                                                                          4493 qaqqqccaecaqatqaaqqaetqcaccqaqcqcaqqqccaacttcctqqqcaaqatctqq 4552
                                                                                                                                            1303 occagodadaggggggggggggaanttretgragagregrergagerearggereer 1362
                                                                                                                                                                                 4553 cocagetaesaagugeegeeeryyeaaettiertyeaqayeeqeeeryyayeresaegyeeeer 4612
                                                                                                                                                                                                                    1363 cooqeeqaqaqetteeqette... qaqqaqaeceareeeqqeeqaqaaqeaqqaq--- 1413
                                                                                                                                                                                                                                       4673 atogacaaaggayrigitacecectgaceag.citgegeagccitgiteggeaaegaeeeeage 4732
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                                                                                                                                                                  Gag-containing polypeptide useful for vaccinating against HTV intections and acquired immunodeficiency syndrome (AIDS) -
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Walker C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV 1; AIDS; Gaq; vaccine; expression cassette; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic HIV Gag/HCV core fusion coding sequence.
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01-PEC-1999;
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qq Š ò ò qq ò qq δλ qq Š 4 709 accaccagraccetgraggagcagategeetggatgaceageaacceccccateeeegtg 768 367 geogocogocaceogocacageageageageageageageageaceategtgeagaacetg 426 caqqqccagatgqtqcaccagqccatcagccccgcaccctgaacqcctgggtgaaggtg 468 487 gtggaggagaaygcettcageeeegaggtgateeeeatgtteagegeeetgagegaggge 546 cagaigeitgaaggacaccaicaacgaggaggecgecgagigggaccgcgigeccgig 648 gacgacatetacaayeggiggateateetyyyeetyääesäägätegigesgatgiacage 828 ggcgagatctacaagcggtgyalcatcctyggcctgaacaagatcgtgcggatgtacagc 846 ecegigagealeciggaealeaageagggeeeeaaggageerloogegaelaegiggae 888 cecaccagoatectggacatecgecagggececaaggagectt.ccgcgactacgtggac 905 301 ctggacaagatcgaggaggagcagaacaagtgccagcagaagatccagcaggccyaggcc 360 307 ctggagaagatcgaggaggaggagcagaacaagtccaagaagaaggcccaggcgccgcc 366 361 geog-----acaaaggcaaggtgagceagaartarrratrgtgragaactg 408 547 gecaecececaggaectgaacaegatgttgaacaeegtgggeggeeaeeaggeegeeatg 606 cagatgetgaaggagaceateaaegaggaggeegeegagtgggaeegegtgeaeeegtg 666 121 ctggagaagttcgccctgaaccccggcctgctggagaccagcgagggctgcaagcagatc 180 181 ateegeeagetgeaeeeegeeetgeagaeeggeagegagagagetgaagageetgtteaae 240 247 accgiggccacccigtactgcgigcaccagegeategaegicaaggacaccaaggaggee 306 427 cagggecagatggtgeaccaggccateageceeegeaceetgaaegetgggtgaaggtg 486 61 elgegeceggeggeaagaagigeiacaigaigaageareiggigigggecageegag 120 67 etgegeereggeggeagaagaagtavaagetuaaueaategtgtgtgtgtgtgtgtgtgtg 127 etggagegettegeegtgaaeeeeggeetgetggagaeeagegagggetgeegeeagate 186 187 ctgggecagetgeageceagectgeagaceggeagegegagegagetgegeageetgtacaae 246 30; Gaps DB 21, Length 2031; 132; Indels Sequence 2041 BP; 421 A; 707 C; 645 G; 257 T; 6 other; 2e-150; 80.9%; Score 1195.8, 89.3%; Fred No. 6 2e iive 0; Mismatches Best Local Similarity 89.3 Matches 1345; Conservative Query Match (AIDS) 409 589 209 787 407 qq qq õ qq $\overset{\circ}{\circ}$ QQ a 10 ò qq οy ÓΥ qq òχ QQ 10 ς ag ya qq Oy Dp δ qq ò δ á ò qq ò

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1387 cccgaggagagettccgcttcggcgaggagaagaccaccccagccagaagcaggagcc 1446
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                                                                                                                                                                                                                                                                                                                                                                                                       1183 ggreacategeegeaactgeegeegeeceegeaa\mathfrak{q}_{\mathfrak{q}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1207 ggecaccaccaggaactyccycychrrngraagaaggetigetggeetgeggeege 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1243 gagggecaccagatgaaggaetgcaccgagegecaggecaactteetgggeaagatetgg 1302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encaquedadaaggeeqeeceggeaactteetgeagageegeeegageecaccgeeec 1362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1363 eccgeegagagetteegette----gaggagaceaeeeeeggeeagaageaggag--- 1413
967 guyaccetyctgytycayaacyccaannnyantgnaagancatnetgaaggntntnynn 1026
                                                                                                  1009 cocygogoccaycotyyayyayyatyattaccgcctgccayyycytyggcyycccayccac 1068
                                                                                                                                                                                                     1069 aaggeeegegtgriggeegäggegatgageeaaggeeaada----eeageqtgatgatg 1122
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                                                                                                                                                       1027 eccycygecaccetygayyayatgatqaregectyneayyynytyyygnyyreneygecac
                                                                                                                                                                                                                                                                                                             1123 cagaagagcaacttcaaggggccccnqqngnatnqtnaagtgcttcaact4cqqcaaggag
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Walker C;
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involved in man, stages of the HTV fle cycle, including assembly, it communition after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recembinant expression of HTV Gag-polypeptides which may then be used to vaccinate
                                                                                                                                                                                                                                                                                The present sequence is the coding sequence of a HIV Gag-protease expression cassette, GagProt.ModS. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is
daq-containing polypeptide useful for vaccinating against BIV
                                                              infections and acquired immunodeficiency syndrome (AIDS)
                                                                                                                                                                 Claim 5; Fiq 7; 491pp; English.
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Sequence 185 (BP) 421 A; 624 C; 580 G; 228 T; 0 other;

against HIV infection and acquired immunodeficiency syndrome (ALDS).

oby cayatychydagyacaccatcaacyagyaggcgccgagtygyaacgcgtgescccqtg 648 6] - ctycycoodgogaagaattactacatgatgaagcanctggtgtggggeeageeggggg-120 12) in Egyadadulit, deen ligadeeseggeet gerliggagaansaggggggggggggggggers 180 307 et ggaagaugategaggaggaggaggagaagteeaagaagaaggeegeegeegee 366 361 gregiiiiiiaaaagagaaaaqagaaaqqtaaacaagaactacceategtgeagaacetg 408 427 cagggecagatggtgcaccaggecateagcecegeaecetgaaegeetgaaggtgaaggtg 486 4.69. atroquagqaaqqoottinaqooqoqqaqqtiqatkooqatqtiicanoqooqtotgaqqqqq-528 523-yin ari cin nayyani tyaavanyahyttyaanaongtyyyddidyyddionaecayyeegeeaty 588 649 canyrogycoreateycorecgycoagatycggegaagacagacagaagaagaagaafegeeggc 708 obl. nacyceyyreceategeereeygecagatyegegaaeeeegegaagaeategeegge 726 709. acciaeraagiamint geaggageagat egeet ggatgaeeageaaeeeeeeat eeeegtig. 768 67 intgegeneeggeggnaagaagaagtacaagetgaageanategtgtgggecageegag 126 467 gengeeggeacogeaacageageageagtgageaagaactaneecategtgeagaanetg 426 7 at grace proceeding the frequency of the same of the 181 latinogenaget geannengeertgragaenggragegagget gaagagnet gitteaae 24] accetturcerectural actiquat quangagaa qaqaqat eqaqqteqacae eaagqaggee 187 etgggecagetgeageeragestyvagaeeggeagegaggagetgegeagetgtaeaae 75.4%; Score 1114.6; DB 21; Length 1853; 85.8%; Pred. No. 3e-139; Live 0; Mismatches 184; Indels 30; (Best Local Similarity 85.8° Matches 1295, Conservative Ouery Match ŝ 5 â 5 ŝ 5 5 3 5 3 Š ŝ 5 = ò ž 5 Ē 5

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HIV Gag professe expression cassette coding sequence GagProtMod.SF2(GPT).
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                                                                                                                                                                                                                                                                                             1009 reeggegeraaretgaaggayatgatgaaregeri geragggegi yqqeygereeagerae - 1068
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                                                                                                                                                                                                                                                                                                                                                                       1069. aaggeeeggetgetggeeggaggegat qageeaggeeaaea.....eeagegtgatgatg 1122
                                                                                                                                                                                                                                                                                                                                                                                       1123 cagaaqaqbaarttcaaqqqqcccccqqcqcatcqtcaaqtqcttcaactqcqqcaaqqaq_1182
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                                                                                                                                                                                                                    949. ganabort gerlagt goggaangebbaan kongan Takabaganat ort gogogotot ogge 1008
                                                                                                                                                                               967 egetletacaagameet pepepetegageaggecagecaggampigaaggaetgaee 966
769. ggegaerat et aesaageggit ggal eat eel gageet gaaesaagat egit gegat git aeage - 828
                                 787. agcqaqatictacaagcqqtqqqqcatictqqqqictqaacaaqatiqtqcqqqtqtataaaqc. 846
                                                                                          889 - gettetteaudaee tues geega geegaag aeeeagaagagaagaagtgatgaeee
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99WO-US 41245.

40-DEC-1999;

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the present sequence is the coding sequence of a HIV Gag protease expression cassette, GagProtMod.SF2 (GPI). The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post:entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may like be used to vaccinate against HIV infection and acquired immunodeficiency syndrome
                                                                                                         Liu H;
                                                                                                                                                                                                Expression cassettes encoding the human inmunodeficiency virus (HIV)
                                                                                                                                                                                                                Gag-containing polypeptide useful for vaccinating against HIV
                                                                                                         Hartog K,
                                                                                                                                                                                                                                     infections and acquired immunodeficiency syndrome (AIDS)
                                                                                                     , Zur Megede J, Srivastava I, Lian Y, Seiby M, Walker C,
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               98US-0114495
                                   99US-0168471
                                                                                                                                                                 WPI; 2000-452400/39.
                                                                      (CHIR.) CHIRON CORP.
                 31-DEC-1998;
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                                                                                                           Barnett S,
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Sequence 1865 BF, 424 A; 627 C, 583 G; 231 T, 0 other,

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469 aleyayyayaayyeelteayeeceyayytyaleeecatyteaceyeeetgagaggg 528
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                                                                                                                                                    61 etgegeeneggeggeaagaagtgetanatgatgaagearetggtgtgggeragergagg120
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                                                                                                                                                                                                                                                                                                                                               193 ctggggccagetgcageccagectgcagaecggcagegaggaggagetgegeagectgtacaae 252
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                                                                         1 algygogocycycvagoaloctgogoggoggoaaqetggacgeetggagogcatecge 60
                                                                                             75,4%, Scute 1114.6, DB 21, Length 1865, 85,8%; Pred. No. 3e-139;
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HTV dag profess expression cassette ending sequence GagprofMed.SF2(GP2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu H;
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                                                                       HIV-1; AIDS; Gag-protease; vaccine; expression cassette; ss
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Greer C, Selby M, Walker C;
                                                                                                                                                   Human immunodeticiency virus type 1.
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qq	1093	anggecegegtgettgecgaggegattgaggecaggtgacegaegaeatgatgaltg
oy ob	1123	caqaagaqcaacttcaagqqccccqqqqqqcatcaattqcttcaactqqqqcaagqaq 1182
Cy Dp	1183	ggodacategeregeaactgeegrqeeereegeaaqaaqqetqetqqqqaaqtqrqqraaq 1242
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qu	1273	qaaqqacaccaaatqaaaqattgcactgaqaqacaqqctaatfttfaqqqqaaqafefqq 1332
č d	1303	occayceacaayyeeyeeeqyaaatteetyeayyeeeeyayeeeyaqooga 1362
s d	1363 1393	cogogogagagettoogettogagaa ancaen ooggeeadaaqaaq 1413
ογ	1414	agraaggaeeegegageeetgaeeeageetgattegaeaegaeeeetg 1470
qq	1453	atagacaaggaactgiateetitaaciteeeteagaleacietitiggeaacgaeeeeteg 1512

Sequence 1865 BP; 460 A; 583 C; 569 G; 253 T; 0 other;

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tive 0; Mismatches 184; Indels 30;
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comprising the coding sequence for a heterologous envelope protein and a third certoviral nucleotide sequence comprising a DNA sequence of interest and lentivirus, preferably HTV, cis acting sequences required for packaging, reverse transcription and integration.
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The packaging cell lines and viral particles can be used for gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.7%; Score 1059.8; DB
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